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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 17:50:45 ; Search time 8647.11 Seconds
(without alignments)
11250.449 Million cell updates/sec

Title: US-09-646-224A-1
Perfect score: 5897
Sequence: 1 ggaagccatcagtgccctga.....gaaaaaaaaaaaaaaaaa 5897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
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32: em.htg_rod.*
33: em.htg_hum.*
34: em.htg_inv.*
35: em.htg_rod.*
36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	5897	100.0	5897	6	AX017217 Sequence
2	5882.6	99.8	5905	10	AF059030 Rattus no
3	5834.6	98.9	5849	10	AJ237852 Rattus no
4	5822.4	98.7	5908	6	E36122 Nucleic aci
5	5295.6	89.8	5334	6	E36125 Nucleic aci
6	4634.2	78.6	5858	10	AF118044 Mus muscu
7	4616.6	78.3	5921	10	AB031389 Mus muscu
8	3242.6	55.0	6237	9	AF188679 Homo sapi
9	3234.2	54.8	6528	9	AF109737 Homo sapi
10	2585.6	43.8	5728	9	AF150882 Homo sapi
11	1414.2	24.0	7823	9	HUMSKMIA
12	1411.4	23.9	6344	10	RNU53833
13	1406.4	23.8	5887	10	MMU278787
14	1405.2	23.8	6527	6	A58859 Sequence 7
15	1403.4	23.8	5523	10	RNY17153
16	1402	23.8	6524	10	RNSNS
17	1401.8	23.8	6957	10	RATNCHVS
18	1399	23.7	6524	6	A58853
19	1386	23.5	5874	9	AF117907
20	1357.6	23.0	6373	10	MMSNS
21	1339.4	22.7	5901	10	AF353637
22	1332.2	22.6	8414	9	AY038064
23	1331	22.6	7545	10	RATSCAL
24	1329.6	22.5	5505	4	ECU25990
25	1327.6	22.5	8491	9	HUMH1A
26	1327.2	22.5	6458	10	MMU271477
27	1311.4	22.2	6726	4	CFU60590
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29	1229.6	20.9	7052	6	A58857
30	1224.6	20.8	5352	10	MMU26707
31	1191.8	20.2	7230	5	EESCP01
32	1191.8	20.2	7230	5	ELCNACH
33	1190.2	20.2	8553	10	RNSCPIIR
34	1183.4	20.1	8552	10	RATNACHI
35	1168.4	19.8	6556	10	AF049239
36	1168.4	19.8	6586	10	AF049240
37	1156.8	19.6	6826	10	RATSCP6A
38	1152.4	19.5	5937	10	AF049617
39	1137	19.3	6822	10	RNSCIII
40	1135	19.2	8398	10	RNSCPIR
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45	1101.4	18.7	7008	9	AB027567

ALIGNMENTS

RESULT 1

LOCUS	AX017217	5897 bp	DNA	PAT	07-SEP-2000
DEFINITION	Sequence 1 from Patent WO9947670.				
ACCESSION	AX017217				
VERSION	AX017217.1	GI:10042137			
KEYWORDS	Norway rat.				
SOURCE	Rattus norvegicus				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 5897)				
AUTHORS	Tate,S.N., Grose,D.T. and Hick,C.A.				
TITLE	Mammalian sodium channel proteins				
JOURNAL	Patent: WO 9947670-A 1 23-SEP-1999;				
FEATURES	YATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS (GB); HICK CAROLINE ANNE (GB)				
Location/Qualifiers	1..5897				

QY 1501 aaaaatccacagctctcttgagcagagaccacaaacgactgtccacagaacttgccagtgagatctc 1560
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Db	3721	AATGSCCTATCTCGCCCTGCTGCAAGTGGCAACCTATAGGGCTGGCTGGAAATCATGAAT	3780
Qy	3781	gctgctgctgattccagagagagaaagacgacgacgcgcggactttgaggcgaaacctctacg	3840
Db	3781	GCTGCTGCTGATTCCAGAGAGAGAAACGACGACGCCGGACTTTGAGGGCAACCTCTACGGC	3840
Qy	3841	tatctctacttctgctgtttttatctcttcgctgctctctttacccctgaacctctttatc	3900
Db	3841	TATCTCTACTTTTGTGGTTTATATCACTTCGSGCTCCTTCTTTTACCCCTGAACCTCTTTATC	3900
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Db	3901	GGTGTATTATTGACAACCTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAGACATTTTT	3960
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Db	3961	ATGACAGAAGAACAGAGAAGAAATTTACAATGCAATGAAAAAGTTAGGAACCAAGAAACCT	4020
Qy	4021	caaaagccatcccaaggccctgaaacaaaagtcaagcctttgttcgacctgggtcaaca	4080
Db	4021	CAAAAGCCCATCCCAAGGCCCTGAAACAAATGTCAAAGCCTTTGTGTGCGACCTGGTGACA	4080
Qy	4081	agccaggtcttgacgtcatcattcgggtctattgtcttaaatatgattatcatgatg	4140
Db	4081	AGCCAGGCTTTGACGCTCATCTCTGGGCTTATTGTGCTTTAAATATGATTATCATGATG	4140
Qy	4141	gctgaatctgcgcagaccagcccaagaatgtgaaagaaaaccttgatatctccaacatagcc	4200
Db	4141	GCTGAATCTGCCAGCAGCCCAAGATGTGAAGAAAAACCTTTGATATCCTCAACATAGCC	4200
Qy	4201	ttcgtgggtcatctttacaatagagtgtctcatcaaaagctttgttcaggagcaacatac	4260
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Db	4381	CGCTTGGCTCGGATTGGTCGAATCTCTCAGAGTGTGTCCGGGCTGCTCCGGGAATCAGGACC	4440
Qy	4441	ctccttctgtttgatgatgtctccctctcttccaacatcgtctcgtcgtcttc	4500
Db	4441	CTCTCTTTGCTTTGATGATGTCTCTCCCTCTCTCTCAACATCGGTCTGTGCTCTTC	4500
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Db	4501	CTGGTGATGTTTCATTTACGCCATCTTGGGATGAGCTGTTTTCCAAAGTGAGAGAGGGC	4560
Qy	4561	tcgggatcgaagacattctcaacttcgagacctttagggcgagcatgctgtgctctcttc	4620
Db	4561	TCGGGATCGACGACATCTTTCAACTTCGAGACCTTTACGGGCAGCATGCTGTGCTCTTC	4620
Qy	4621	caagataaccacttcggctggtcgggataccctcctcaaccccatgctggaggcaagaaga	4680
Db	4621	CAGATAACCACTTCGGCTGGCTGGGATACCTCTCTCAACCCCATGCTGGAGGCAAAAGAA	4680
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Db	4681	CACTGCAACTCTCTCTCCCAAGACAGCTGTTCAGCAGCGCGAGATAGCCGTGCTACTTTC	4740
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Db	4981	T TTCAGTTTTCTAGTGATGACTTGCCCATGGTGATGGCGCACCCCTCCATTGCATGGAT	5040
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QY	5101	accatgatgagagagaagtttatggagggccaacccttttaaagaagctcttacgagcccata	5160
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QY	5161	gtcacacacaccaagaggaagagagagcaaggcgccgcgtcatccagagggcctac	5220
Db	5161	GTCACCAACCAAGAGGAAGGAGGAGGAGCAAGGCGCCGCTCATCCAGAGGGCCTTAC	5220
QY	5221	cggaaacacatggagaagatggtcaaacctgagggctgaaggacaggttcaagtgtcatcgcac	5280
-Db	5221	CGSAAACACATGSGAAGATGTTCAAACCTGAGGCTGAAGGACAGGTCAGGTTTCATCGCAC	5280
QY	5281	csagggttttgcaatggacaacttgcagacttgatgtggccaaggttcaaggttcaaat	5340
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QY	5341	gactgaacctcatctccacctactcactgctctcagacttagcctccagcctctg	5400
Db	5341	GACTGAACCTCTCATCTCCACCCCTACTCTACTGCCCTCAGCTTAGCCTCCAGCCTCTGG	5400
QY	5401	cgagcaggcggcagactcactgaacacagggcgttcgatctctgtgttttggctgaacag	5460
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QY	5461	gtgacaggttgcggtccatttttaaatgactcttgaaaagatttcaatgtagaagatggtt	5520
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Db 1564 TTTGATGAGCACCTGTGACCCCTCCACAGCAGAGAGCGGTGAGCGCTGTACATCTTA 1623
QY 1621 accatcacatatacaggaacaaagaaaattccagagagccttgtttcccatgtgggaaaaat 1680
Db 1624 ACCATCACATGCAGGAACAAAGAAAAATTCAGGAGCCTTGTGTTCCCATGTGGGAAAAAT 1683
QY 1681 ttggcctctaagtacatcgtgttgagacttagccctcagtggtgtgcataaagaggtc 1740
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QY 1741 ctgagacatcatgacgatccctttactgagctgagcattcacatcgtcatcatc 1800
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Db 1804 AATACCGTTTTCTTAGCCGTGGAGCACCACAACATGSATGACAACTTAAGACCATACTG 1863
QY 1861 aaaaatggaactgggttttttcacgggaatttccatgcgggaatgtgtctcaagatc 1920
Db 1864 AAAATAGGAAACTGGGTTTTTCAGGGGAATTTTCATAGCGGAAATGTGTCTCAAGATCATC 1923
QY 1921 ggcctcagaccttaccactacttccggcagcgtgaaatgtttttgacagcagctggcc 1980
Db 1924 GCGCTCGACCTTACCACACTACTTCCGGCAGCGGTGGAATGTTTTTTCACAGCATCTGGCC 1983
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Db 3004 AAAAGAGTTTCCCCCAAAAAGCAGCAGATAGATGCTTTTCCCCAAGGGCTTGTGTTGTCAC 3063
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Db 3064 TTTCTATGCCACAAAACAGACAAAGTCCCTCTGGGTCTCTGGTGGACATTCGG 3123

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Db	3124	AAAACCTGCTACCAAATCGTGAAGCACACAGCTGGTTGTGAGAGTTTTCATAAATCTTTGTGTTATT	3183
Qy	3181	ctgctgagcagtgagcgcgtgatatattgaagatgtcaactcccccagcggcccccgaagtt	3240
Db	3184	CTGCTGAGCAGTGGAGCGCTGATATTTGAAGATGTCAATCTCCACAGCGCGGCCCAAGTT	3243
Qy	3241	gagaaattactaaagtgtagcccaataattttcacattattttccctcctggaaatgac	3300
Db	3244	GAGAAATTACTAAGGTGTACCGATAAATTTTTCACATTTATTTTCCCTCGGAAATGATC	3303
Qy	3301	ctgaagtgggtggcctttggattccggaggtattttccaccagtgctcgtgctggcttgat	3360
Db	3304	CTGAAGTGGGTGGCCTTTGGATTCCGGAGGTATTTTACACAGTGCCTGGTCTGGCTTTGAT	3363
Qy	3361	ttcctcaattggtggtgctgctgctcagctcatgaatctaccaaagcttgaagtccttc	3420
Db	3364	TTCTCTCATTTGGTGGTGCTGTGCTCAGTCTCATGAATCTACCAGACTTGAAGTCTTTC	3423
Qy	3421	cggactcggggccctgagacctcggggcgctgctcccgagtttgaaggaatgaaggtt	3480
Db	3424	CGGACTCTGGGGCCCTGAGACTCTGCGGGCGCTGCCAGTTTGAAGGAATGAAGGTT	3483
Qy	3481	gtgctcagccctgatacagccataacctgccattctcaatgctctgctggtcgtgcctc	3540
Db	3484	GTGCTCTACGCCCTGATCAGCGCCATPACCTGCGCATTCCTCAATGTCTTGTCTGGTCTGCCTC	3543
Qy	3541	attcttggctcgtaatttggatccttgggagtaaatatttctctgggaagtttgggaag	3600
Db	3544	ATTTTCTGGCTCGTATTTTGTATCTTGGGAGTAATTTATTTTCTGGGAGTTTGGGAAG	3603
Qy	3601	tgoattaacgggagacataaataatgtatttggatttaccgaagttccgaaaccgaagc	3660
Db	3604	TGCATTTAACGGGACAGACATAAATATGTATTTTGGATTTTTCGGAAGTTTCGAAACCGAAGC	3663
Qy	3661	caatgaacattagtaattactcgtgggaagtcctcgaggtccacacttggacaacgtggg	3720
Db	3664	CAATGTAACATTTAGTAATTTACTCTGTGGGAAGTCCCGCAGGTCAACTTTTGACACGCTGGG	3723
Qy	3721	aatgcctatctgcctcgtcgaagtggcaacctataagggtcgtggctggaaatcatgaat	3780
Db	3724	AATGCCTATTCTGCCCTGTGCAAGTGGCAACCTTATAAGGCTGCCTGGAAATCATGAAT	3783
Qy	3781	gctgctgcattccagagagaaagacagcagccggactttgaggcgaaacctcagcg	3840
Db	3784	GCTGCTGCGAATTCAGAGAGAAGACGAGCAGCGGACCTTTGAGGCGGAACCTCTACGCG	3843
Qy	3841	tatctcactttgtggttttatcatcttcgctcctctcttaccctgaacctctttac	3900
Db	3844	TATCTCTACTTTGTGTTTTTATCATCTTCGGCTCCTTCTTTTACCCTGGAACCTCTTTATC	3903
Qy	3901	gggtgtattattgacaacttcaatcagcagcagaaaaagtttagtggccgaagacattttt	3960
Db	3904	GGTCTTTATTATGACAACTTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAGACATTTTT	3963
Qy	3961	atgacagaagaaacagaagaaaaattacaatgcaatgaaaaagtttagaaccacaagaacct	4020
Db	3964	ATGACAGAAGAACAGAAATAATTAACAATGCAATTGAAAAAGTTAGGAACCAAGAAAACCT	4023
Qy	4021	caaaagcccatccaaagccctgaacaaatgccaagcctttgctcgacctggtcac	4080
Db	4024	CAAAAGCCCATCCCAAGGCCCTTGAAACAATGTCAAGGCTTTGTGTTCGACCTGTCACA	4083
Qy	4081	agccaggtctttgacgtcatctattgggtcttattgtcttaaatatgattatcatgatg	4140
Db	4084	AGCCAGGCTCTTTGACGTCTATCTCTGGGCTCTTATTGCTTTAAATATGATTTATCATGATG	4143
Qy	4141	gctgaaatcctgcagacagcccaaaagatgtgaagaaaaacctttgatatactcaacatagcc	4200
Db	4144	GCTGAATCTGCCACACGCCCAAGATGTGAAGAAAACCTTTGATATCTCTCAACATAGCC	4203

Qy	4201	ttcgtgggtcaatctttaccatagagtgtctcatcaaaagtcttctgttgaggcaacatac	4261
Db	4204	TTcGTGGTcATcTtTTAcCATAGAGTGTcTcATCAAAgTCTtTTGcTTTgAGGCAACAcTAc	4263
Qy	4261	ttcaccaatggcttgaaacttatattgaatgtgtggtcgttggtttcttctatcattagtacc	4320
Db	4264	TTcACCAATAgGcTgGAACATtTTGATgTGTgGTGTgGTgTCTTCTATcATTAGTATCC	4323
Qy	4321	ctggtttcccgcgttgagagacagtgcacattttttccgcgcacgcgtctctcagagtgcgc	4380
Db	4324	CTGgTtTCCGcTtTGAGGAcAGTgCATtTCTTCCCGCCAcGCTCTTcCAGAGTcGTc	4383
Qy	4381	cgcttggctcggaattggtcgaaatcctcaggtcgtgtcccggtgcgccgggggaatcagaacc	4440
Db	4384	CGcTtGGcTcGGAATtGGTcGAATcCTcAGcTGTgTcCGGGTGTcCCGGGAATcCAGAcC	4443
Qy	4441	ctcctcttgcttgatgatgtctctccctctctcttcaacatcgctctgctactcttc	4500
Db	4444	CTcCTcTtTGTtTGATGATgTCTCTCCcCTCTCTCTcAACATcGGTCTcGTcCTCTTC	4503
Qy	4501	ctggtgatgttcattacgcacatctttgggatgagctggtttttccaaagtgaagaaggcc	4560
Db	4504	CTGgTGATgTTCATtTAcGCCATcTtTGGATgAGcTGTgTTCcAAAGTGAAGAAGGc	4563
Qy	4561	tccgggatcgaacacatctctcaactctcagacacttaccgggcagatcgtctgctcttc	4620
Db	4564	TcCGGATcGAcGAcATcTtTCAAcTtTcGAGAcCTtTAcGGcGAcGATcGTcGTcCTCTTC	4623
Qy	4621	caataacacacttcggctggctggatgccctctcccaaccatgcctgagagcaagaagaa	4680
Db	4624	CAGATAAcCATtTcGGcTGGcTGGATAcCCCTCTCTcAACCCcATcGTcGAGGCAAAAGAA	4683
Qy	4681	cactgcgaactcctctcccaagacacagctgtcagcagccgcgcagatagccgtcgtactctc	4740
Db	4684	CACtTGAACtTCCtCCtCCcAAGAcAGcTGTcAGcAGcCGcAGATAGcGTcGTcACTTC	4743
Qy	4741	gtcagttacaatcatctctctctctcatcgtgtgtgttcaacatgtacaatcgtgtgatacctc	4800
Db	4744	GTcAGTtTAcATcATcATcTCTCTCTcATcTGTGTgTGTCAAcATGTATcATcGTcGTcATcCTc	4803
Qy	4801	gagaacttcaacacagccacgagagagacgagagaccctctggagagagacacttgaa	4860
Db	4804	GAGAAcTtTCAAcACAcCCAGGAGAGAcGGAGAcCCCTCTGTGGAGAGAcGAcTtTGAA	4863
Qy	4861	atctctcatgagctcgtggagaagtttgaccgccgagcgctgcgcagtctcatccagattcgc	4920
Db	4864	ATcTCTATAGGTcTGGGAGAAGTtTGAcCCcCGAGGcGTcGCAGTtCATcCCATATcCG	4923
Qy	4921	gccctctcgaacttcttggaacccctgcgcgagccgttgcgtgtggccaagccgaataag	4980
Db	4924	GCcCTCTcTGAcTtTcGGAcCGcCTTcCGGAGcCGTtTGCgTGTgTGCcCAcCAATAAg	4983
Qy	4981	tttcagtttctaagtatgaacttgcccatgtgatggcgagaccgcctccattgcatggat	5040
Db	4984	TtTcAGTtTCTAGTGTATGAcTtTGCCATGTGTgATGGcGAcCGcCTCTcATTGTcATGGAT	5043
Qy	5041	gtctctttgcttctactaccagggttcctcggggagactccagcgctctggataccatgaag	5100
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Qy	5101	accatgatggaggagaagtttatgtagggccaaccccttttaagaagctctcagagcccata	5160
Db	5104	AcCATGATGAGGAGAAGTtTATGGAGGcCAAcCCCTTtTAAAGAcTCTAcAGAGCCcATA	5163
Qy	5161	gtcaccaaccaagaagagagagagagcaagcgccgcgtcatccagagggccctac	5220
Db	5164	GTcACcACcCAcCAAGAGAAgAGAGAGAGAcAAAGcCGcCGcGTCTAcCAGAGGGcCTAc	5223
Qy	5221	cgaataacatgagaagatgtctaaactgagctggaagcagaggtcaagtctcatcgcac	5280
Db	5224	CGGAACAcATGAGAGAAGATGTCTAAAcTGTAGGcTGTAGAGAcAGGTcAAGTtTcATcGCAC	5283
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Db 361 TTAATGATTCGTATCTCTGTCATTAGCTCTTATGATGTTTCATCATCTCAGCGGTGATC 420
QY 469 atcaactgtatgttcatctggtcgaattctctatgagagaagttctcagacaacgacatcccgaa 528
Db 421 ATCAACTGTATGTTCATGCGGAATCTTATGGAGAGAAGTTTCGACAAACGACATTCGCGAA 480
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Qy	2619	agaaagcttctgctggtgagaaataaagactcaatctcccgatcgagggccctggaagga	2678
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Qy	2679	gtatgatacagaacatggtttgtacactggacagccggggtccgctgcccactcgc	2738
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Qy	2739	agaggtagaggacgatgagaaatatgttggtgaaggcgtgccctaccacactcaaca	2798
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Qy	2799	tagtgcctggagttcagggccggtgacctccctccagagaccagcagctcactagccgga	2858
Db	2829	TAGTGTGGAGTTTCAGGCCGCTGACCTCCCTCCAGAGACCAAGCAGCTCACTAGSCCGGA	2888
Qy	2859	tgaccaaggggtgaaatggaagtatttctgaaagaagatctgcatttaagcatacagag	2918
Db	2889	TGACCAAGGGGTTGAAATGGAAGTATTTTCTGAAGAAGATCTGCACTTAAAGCATACAGAG	2948
Qy	2919	tcctcgaagaagctctgcgcagtgagcatgctcgcgaatgcagcacaaattgaacctgaa	2978
Db	2949	TCCTCGAAGAGACTGACGCGAGTGAGCATGCTCTCGGAATGCAAGACAAATTGACCTGAA	3008
Qy	2979	tgatatctttagaaattacagaaacaggtttcccccacaaaagcagccagatagatgctt	3038
Db	3009	TGATATCTTTAGAAATTTACAGAAAACAGTTTTCCTCCCAAAAAGCAGCCAGATAGATGCTT	3068
Qy	3039	tcaccaaggccttagtgttcactttctatgcacaaaaacagacagaagagaagtcctccctg	3098
Db	3069	TCCCAAGGGCTTAGTGTGTCACTTTCATGCCCACAAAAACAGACAGAAGAGTCCCCCTG	3128
Qy	3099	ggctcctggtggaacattcgaaaaacctgctaccaaaatcgtgaagcacagctggtttga	3158
Db	3129	GGTCTGTGTGGAACATTTCGGAANAACCTGTCTACCAATCTGTGAAGCACAGCTGGTTGA	3188
Qy	3159	gagttcataactcttgttatctctgctgacgagtgagcgtgatattggaagatgcaa	3218
Db	3189	GAGTTTCATAATCTTTGTTATTCTGCTGAGCAGTGGAGCGCTGATATTTGAAGATGTCAA	3248
Qy	3219	tcctccacagccggcccaagttgagaaattactaagggtgtaccogataatatattcacatt	3278
Db	3249	TCCTCCACAGCCGCCCAAGTTGAGAAATTTACTAAGTGTACCGGATATATTTTTCACATT	3308
Qy	3279	tatttctctggaatagatcctaagtggtgaccttgatctggattccgaggtatttcac	3338
Db	3309	TATTTTCTCTCGAAATGATCCTGAAGTGGGTGGCCCTTTGGATTCGGAGGATTTTCAC	3368
Qy	3339	cagtgcctgctgctgctgatttccctcattgtggtggtctgtctgtcagctctcagaa	3398
Db	3369	CAGTGCCTGTGTGCTGCTTGATTCTCTCAATTTGTGTGTGTCTGTGTCTCAGTCTCATGAA	3428
Qy	3399	tcaccaagcttgaagtccttcogactctgcgggacctgagacctctgagggcgctgctc	3458
Db	3429	TCTACCAAGCTTGAGTCCCTTCGGACTCTCGGGCCCTGAGAGCTCTCGGGCGCTGTC	3488
Qy	3459	ccagtttgaaggaaatgaaggttgtcgtctaagccctgatcagcccatacctgccattct	3518
Db	3489	CCAGTTTGAAGGAATGAAGGTTGTCTGTACGCCCTGTATCAGGCCCATACCTGCGCATTCT	3548
Qy	3519	caatgtctgtcgtctgcctcatttctcgtctglattttgtatctctggagatgaatt	3578
Db	3549	CAATGTCTGCTGGCTCGCCTCATTTTCGGCTCTGATTTTGTATCTTTGGAGTAAATTT	3608
Qy	3579	atttctctgggaagtttggaaggtgcattaaacgggacagacataaatatgtatttgattt	3638

Db	3609	ATTTCCTGGGAAGTTTGGAAAGTGCATTAAACGGGACAGACATAAATATGATTTGGATTT	3669
Qy	3639	taccgaagtccgaaccgaagaaccaatgtaacctagtaattactcgtggaaggtcccgca	3698
Db	3669	TACCCGAAGTTCGAAACCGAAGCCANTGTAAACATTAGTAATTA	3728
Qy	3699	ggctcaacttggacaacgtggggaaatgcctatctcgcctcgtcgaagtggcaacctataa	3758
Db	3729	GGTCAACATTGTGACAAAGTGGGAAATGCCCTATTCTGCCCTTGC	3788
Qy	3759	ggcctggcgtgaaatcatgaatgctgcgtgcgatccagagagaagaacagcagccgga	3818
Db	3789	GGCGTGGCTGGAAATCATGAATGCTGTCGATTCCAGAGAGAAGACGACGACGGGA	3848
Qy	3819	ctttgagcgcaacctctacgcgtatctctcaacttctgtggttttatactctcgcgtccctt	3878
Db	3849	CTTTGAGCGGAACCTCTACGCGTATCTTACCTTTGTGGTTTTTATCATCTTCGGCTCCTT	3908
Qy	3879	ctttaccctgaacctcttttatcgggtgtttattattgacaacttcaatcagcagcagaaaa	3938
Db	3909	CTTTACCCTGAACCTCTTATTCCGGTGTATTATTGACAACCTTCAATCAGCAGCAGAAAA	3968
Qy	3939	gttaagtggccaagacatttttatgacagagaagaagaataattacaatgcaatgaa	3998
Db	3969	GTTAGGTGGCCAAAGACATTTTATGACAGAGAAGACAGAANAATATTACAATGTCAATGAA	4028
Qy	3999	aaagttaggaaccaagaacacctcaaaagcccatcccaagggcccttgaaacaatgtcaagc	4058
Db	4029	AAAGTTAGGAACCAAGAAACCTCAAAAGCCCATCCCAAGGCCCTTGAACAAATGTCAAGC	4088
Qy	4059	ctttgttctggaccttggtcacaaagccaggtctttgacgtcatcttctgggtcttattgt	4118
Db	4089	CTTTGTGTTCGACCTGGTCACAAGCCAGGTCTTTGACGTGTCATCTTCTGGGTCTTATTCT	4148
Qy	4119	cttaaatatgattatcatgatggttgaaatctgcgacacagcccaagaagatgtgaagaaaac	4178
Db	4149	CTTAATAATGATTATCATGATGGCTGAAATCTCCGACACAGCCCAAGATGTGAAGAAAAC	4208
Qy	4179	ctttgatatctcaacatagcctcgtggtgcatctttaccatagagtgtctcatcaaaagt	4238
Db	4209	CTTTGATATCTTCACATAGCCTTCTGTGTCATCTTTACCATAGAGTGTCTCATCAAAGT	4268
Qy	4239	ctttgctttgaggaacactacttccaaatggctgggaacttatttgattggtggtcgt	4298
Db	4269	CTTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTGATTGTGTGTCGT	4328
Qy	4299	ggtttctttatcatagtaacctgggtttccgcttggaggacagtgaacatttcttccc	4358
Db	4329	GGTCTTTCTTATCATTTAGTACCTGGTTTCCGCGTGGAGGACAGTACATTTCTTTCC	4388
Qy	4359	gcccaagcctctcagagtcgtccgcttggctcgagttggtcgaaacctcagcgtggtccg	4418
Db	4389	GGCCACGGCTCTTCAGAGTGGTCCGCTTGCGATTGGTTCGAATCCTCAGGCTGGTCCG	4448
Qy	4419	ggctgcccgggaaatcaggacacctctcttcttttgatgagtctctccctctctctt	4478
Db	4449	GGCTGCCCGGGAAATCAGSACCTCTCTCTTTGATGATGTCTCTCCCTCTCTCTCTT	4508
Qy	4479	caaatcggctcgtcgtcttctcgttgatgttcaattacgccaatcttgggatgaagctg	4538
Db	4509	CAACATCCGCTCTGCTGCTCTTCCTGGTGATGTTCATTTACGGCATCTTTTGGGATGAGCTG	4568
Qy	4539	gttttccaaagtgaagaaggcctccggatcgacacatcttcaactcgaacctttac	4598
Db	4569	GTTTTCAAAGTGAGAGAGGGCTCCGGGATCGAGACATCTTCAACTTCGAGACCTTTAC	4628
Qy	4599	gggcagcatgctgtgctcttccagataaccacttcggtcggtcggtgggaacctctctaa	4658
Db	4629	GGGAGCATGCTGTGCTCTTCCAGATAACCACTTCCGCTGGGTGGGATACCTCCTCAA	4688
Qy	4659	ccccatgctggaggcaaaagaacatgcaactctctctcccagaacagctgtcagcagcc	4718
Db	4689	CCCATGCTGGAGGCAAAAGACACTGCAACTCTCTCCCAAGACAGCTGTTCAGCAGCC	4748

Qy	339	aagaaacatttatcgcttcagcgccgaagcgggccccttgctcattctggggcccttttaatcc	398
Db	314	GAGAACAAATTTATCGCTTCAGCGCCAAGCGGCCCTTGTTTCATTCTGGCGCCTTTTAAATCC	373
Qy	399	cctcagaagcttaaatgattcgtatctctgtcctcattcagctctttagcatgtttcatctctg	458
Db	374	CCTCAGAAGCTTAATGATTCGTATCTCTGCTCCATTTCAGCTCTTTAGCATGTTTCATCATCTG	433
Qy	459	caeggtgatcatcaactgtatgttcatggcggaattcttatgtagaagctgtgataaataattggc	518
Db	434	CACGGTGATCATCAACTGTATGTTTCATGCGCAATTCATTGAGAGAAAGTTTCGACAACGA	493
Qy	519	cattccggaatacgtcttcattgggaatttatattttaagaagctgtgataaataattggc	578
Db	494	CATTCCCGAATACGCTCTCATTTGGGAATTTATATTTTGAAGCTGTGTATTAATAATTTGGC	553
Qy	579	aagaggctcatgttggaatgagtttccctctcccgagatccgctggaaactggctggagactt	638
Db	554	AAGAGGCTCATTTGTSATGAGTTTTCTTCCTCCGAGATCCGTGGAACTGCGCTGGACTT	613
Qy	639	cattgtcaattggaaacagcgatcgcaacttgctttccggcgagccaaagtcaatctttcaagc	698
Db	614	CATTGTCTATTTGGAACAGCATCGCAACTTGTTTTCCGGCGCAGCCAAGTCAATCTTTCA	673
Qy	699	ctctcglacctcccgagtgcttcagagctctgaagcgcatttcagttactcagactcagaa	758
Db	674	TCCTTCGTACCTCTCCGAGTGTTCAGAGCTCTGAAGCGGATTTTCAGTTATCTCAGGCT	733
Qy	759	ggctcatcgttagtgccctgcctgcctgcgtcgaggaagctggtagacgtgagtgcctcac	818
Db	734	GGTCATCGTAGTGCCTGCTGCTGGCTCGGTGAAGAAGCTGGTAGACGTGATGGTCCCTC	793
Qy	819	tcctctctgcctcagcatctcttgccctgctggctcagcagctgttcatcgggaattctgaa	878
Db	794	TCTCTCTGCGCTCAGCATCTTTGCCCTGCTGGCTCAGCAGCTGTTTCATGGGAATCTGAA	853
Qy	879	ccagaagtgtattaagcacaaacttgcccacccctgcattcccaacaaggaattccttga	938
Db	854	CCAGAAGTGTTATTAAGCACAACTGTGGCCCCAACCCCTGCATCCACAAGGATTCGTTGA	913
Qy	939	aaeggaanaagatagcgaagacttcataatgttggttacctggctcgcgacgacagaccctg	998
Db	914	AAAGGAAAAAGATAGCGAAGACTTTCATAATGTGTGTTACCTGGCTCGCGACGACCCCTG	973
Qy	999	tcocaaatgggttctactgtggaataaaaccacatgaagccagacacataataatacaagtt	1058
Db	974	TCCCAATGGTTCTACGTGGCGATAAAACCCACATTGAACCCAGACAAATAATTACAAAGTT	1033
Qy	1059	tgacaacttggctggctctctcgcacgtctccgggttatgactcaagactcctggga	1118
Db	1034	TGACAACCTTTGGCTGGTCCCTTCTGCCCATGTTCCGGGTATGACTCAAGACTCCTGGGA	1093
Qy	1119	gaggtctttacgcagacatcctcggaacctctgggatactattgtctctctctcttggt	1178
Db	1094	GAGGCTTTACCGACAGATCCTGGGACCTCTCGGATCTACTTTGCTTCCTTCCTGGT	1153
Qy	1179	ggctcatctcctgggtctctctactcgtcttaacctaacctcgcgtttgttccacctatggc	1238
Db	1154	GGTCATCTCCTGGGCTCTCTTACCTGCTTAACTTAACCTAACCCCTGGCTGTGTGCACATGGC	1213
Qy	1239	ttatgaagaacagaacagaaatgactgctagacagagcccaagagagaaatgtttca	1298
Db	1214	TTATGAAGAACAACAAGAAATGACTGCTCAGACAGAGGCCAAGGAGAAATGTGTTC	1273
Qy	1299	ggaagccagcagctgtttaaggggagagaaaggaggtcctgtgtgccaatgggaattgacag	1358
Db	1274	GGAAGCCACGACGCTGTTAAGGAGGAGGAAGGAGGCTCTGTTGGCCATGGCAATTCAG	1333
Qy	1359	aagtctccttaattcctctcaagcttcactcttttcccccgaagaagaggttttctcg	1418
Db	1334	AAGTTCCTTAATTCCTCTCAAGTCTTCATCTCTTTTCCCGAAGAGAGAGTGTTCGG	1393

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1479	tgattcagagacatgcctctctaaaatccacagctccttgagcagacaacaacacactgct	1538
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1514	CCAGAACTTGCCAGTGGATCTCTTTGATGAGCAGCTGGAGCCCTCCACAGCAGAGAGC	1573
1599	gctgagcgctgctcagtatcottaaccatcaccatatacaggaaacaagaaaaattccaggagcc	1658
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1659	ttgtttcccatgtgggaaaaatttggcctctaagtaccttggctgggagctatgacctca	1718
1634	TTGTTTCCCATGTGGGAAAAATTTGGCCTCTAGTACCTGGTGTGGGACTGTAGCCCTCA	1693
1719	gtggctgtgcataaagaaggtcctgggacccatcatgacggaatcccttactgagctggc	1778
1694	GTGGCTGTGCATAAAGAAGGTCTTGGCGGACCATCATGACGGATCCCTTTACTGAGCTGGC	1753
1779	catcaccatctgcatcatcatcaataccgttttcttagccgttgagagacacacaacatgga	1838
1754	CATCAcCATCTGCACTATPACATACCGTTTTCTTAGCCGTGGAGCACCACAACATGGA	1813
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1899	ggaaatgtgtctcaagatcatcgcgctgcaccttaccactacttccggcacggtcgaa	1958
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1934	TGTTTTGACAGCATCGTGGCCCTCCCTGAGTCTCGCTGATGTGCTACTAACACACACTGTC	1993
2019	tgataacaataggctcttcttgctccctcagagtgctgaaggtctctcaagttagcaa	2078
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2199	cittcggtaccagtttaacaagacgcctacgcacccagagcggcccaaggcggcgctg	2258
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Qy	2491	agaaacaaagtgcagctagccctggatcggttccgcgcgggccttctccttcactgctg	2550
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Qy	2551	caagctcttcagagttttgttgcagaagaaatgcagggaggaaaaaactcgcacaaagccaaaa	2610
Db	2558	CGCGCTCTTCAGAAATTTCTGTTGCAAGAGATGCAAGAGGCAAACTCGCCAAAGCCAAAT	2617
Qy	2611	gagacacagaagccttgcctggtgagataaagactcaaactccctccgcgagtcgagggccc	2670
Db	2618	GAGCAACAGAAAGCTTGCTGGTGAGAGTACAGACACAGCCACCCCTGGATACAAAGTGCC	2677
Qy	2671	tggaaggagtatgatacagacatggctttgtacactggacagcgccggggctccgcctggcc	2730
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Nat/Scnlla, complete cds.
ACCESSION
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VERSION
AB031389.1 GI:7024452
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voltage-gated sodium channel alpha subunit Nat/Scnlla.
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (sites)
Ogata,K., Jeong,S.Y., Murakami,H., Hashida,H., Suzuki,T.,
Masuda,N., Hirai,M., Isahara,K., Uchiyama,Y., Goto,J. and
Kanazawa,I.
Cloning and expression study of the mouse tetradotoxin-resistant
voltage-gated sodium channel alpha subunit Nat/Scnlla
Biochem. Biophys. Res. Commun. 267 (1), 271-277 (2000)
2 (bases 1 to 5921)
Ogata,K., Jeong,S., Goto,J., Murakami,H., Hashida,H., Suzuki,T.,
Masuda,N., Hirai,M., Isahara,K., Uchiyama,Y. and Kanazawa,I.
Submitted (23-AUG-1999) to the DDBJ/EMBL/GenBank databases.
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BASE COUNT 1530 a 1447 c 1396 g 1548 t
ORIGIN

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Matches 5183; Conservative 0; Mismatches 614; Indels 78; Gaps 12;

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RESULT 10
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DEFINITION Homo sapiens voltage-gated sodium channel alpha subunit, alternate
splice variant SCN12A-s (SCN12A) mRNA, complete cds.
ACCESSION AF150882
VERSION AF150882.1 GI:6693704
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5728)
AUTHORS Jeong, S.-Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N.,
Hirai, M., Isahara, K., Uchiyama, F., and Kanazawa, I.
TITLE Identification of a novel human voltage-gated sodium channel alpha
subunit gene, SCN12A
JOURNAL Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
MEDLINE 20090626
REFERENCE 2 (bases 1 to 5728)
AUTHORS Jeong, S.-Y., Suzuki, T., Hashida, H., Ogata, K., Masuda, M., Goto, J.,
and Kanazawa, I.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1999) Neurology, Graduate School of Medicine,
Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan
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ORIGIN

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3'UTR
BASE COUNT 1621 a 2354 c 2147 g 1701 t
ORIGIN Chromosome 17q23.1-25.3.

Query Match 24.0%; Score 1414.2; DB 9; Length 7823;
Best Local Similarity 57.6%; Pred. No. 0;
Matches 3007; Conservative 0; Mismatches 2093; Indels 117; Gaps 22;

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QY	154	g---agagggaagttccaaagacaagcgcgagctgagccccagcctcgccctcagctt	210
DB	186	GCCCGGCTGCAGCGGAATAGCAGATGAGATTGAGGAGCCCGACGAGCCACGAGT	245
QY	211	gacctaaagcctccaggaagttacctaaagctttatggtgacattccccctgagctgtt	270
DB	246	GACTTGGAGGCTGCAAGAAGACCTACCATGATCTACGAGACCCCGCGGGAGGTATC	305
QY	271	acgaacctctgaggaacctggaccctactataaagaacataagaacattcaggtgtg	330
DB	306	GGCATCCCTCTGGAGGACCTTCCGCTTCTCCGCCACACCTGCTCTCTACCTGCTGACTC	365
QY	331	aacaagaaagacaatttatcgttcagcgccaagcgccctgttcttcattctggggcct	390
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QY	391	tttaatccccctcagaagcttaagattcgtatctctgtccattcagctcttagcatgtc	450
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QY 4120 ttaaatatgattatcatgattggtgatttgcgaccagcccaagaatgtggaagaaacc 4179
Db 4170 CTCAACATGTGTCACCATGATGTTGGTGGAGACAGACAGACAGGCCAGGCTCAAGGTTGACATC 4229

ILQMDLPLVPGDKIHCLDILFAFTKNVLGCEGSELDLKTNMEEKPMATNLSKASTEP
IATILRWKQDSATVIOKAYRISLMJHRSUTLSNTHVPRAEEDGVSLPGEKVTTMA
NSGLPKSETASATPQKSYDVSYRGLSDRANINPSSMQNEDVAAKEGNSPQ"
1487 a 1823 c 1622 g 1412 t
BASE COUNT
ORIGIN

BASE COUNT	1487 a	1823 c	1622 g	1412 t
ORIGIN				

Query Match 23.9%; Score 1411.4; DB 10; Length 6344;
Best Local Similarity 57.6%;
Matches 3248; Conservative 0; Mismatches 1921; Indels 474; Gaps 21;

Qy 45 gaagatggagagagggtactaccgggtgattcttccccggagcagcggaaatttccgcctt 104
Dy 10 GAAGAATGAGAAAGATGGAGCTCTCCCTTTGGCTCGGTGGGAACTACCAATTTTCAGACGGTT 69
Qy 105 cactccgactctcgctgcctataaagaagcgatgctatccaa-----aa 152
Dy 70 CACTCCAGAGTCACTGGCAGAGATCGAGAACGATGTCTGCTCACCGCGCAGCCAGAA 129
Qy 153 ggagagaagaagtcctccaaagaaggcgagcgtgagcccgactcgtggcctcagcttga 212
Dy 130 GGCCAGAACCAAGCACAGAGGACAGGAGCAAGGGCGAGAACCCAGGCCCTCAGCTGGA 189
Qy 213 cctaaaggcctccagggaagttaactaagcttattggtgaacttccccctgagctgttac 272
Dy 190 CTTGAAAGCTGTAAACAGCTGCCCAAGTCTATGTGTGAGCTCCAGCAGAACCTGGTCGG 249
Qy 273 gaacctctggagacctggaccctactcaagaagaccataagaacattcatggtgtgaa 332
Dy 250 GGAGCCCTGGAGAACCTAGACCCCTTCTACGACACACCGGACATTCATGTGTGTGAA 309
Qy 333 caagaaaagaacaattatcgcttcacggccaaaggcgcttcttcattctgggcccctt 392
Dy 310 TAAAGCAGGACCATTTCAGATTTCAGTGCCACTTGGGCCCTGTGGCTCTTCAGTCCCTT 369
Qy 393 taatccctcagaagcttaagtattgattatctctgtccattcaagcttcttaagcttcaat 452
Dy 370 CAACCTGATGAGAAAGACAGCCATCAAGTGTCTGTCCATTTCCTGGTTCCTCATTTTCAT 429
Qy 453 catctgcacggtgatcataactgtatgttcattgacggcaattctatggagagaagttcga 512
Dy 430 CACCATCACTATTTTGGTCACTCGGTGTGATGACCC-----GAACGTGATCT 477
Qy 513 caagacattccgaatactgtcttoattgggatttatatttagaagctgtgattaaaaa 572
Dy 478 TCCAGAGAAATCGTAGTACGCTTCACCTGTCTATTATACACCTTCGAGGCTCTGATTAAAT 537
Qy 573 attgcaagagcttcattggtgatgatttctctccgaatccgtgagaactgct 632
Dy 538 ACTGCGAAGAGGGTTTGTCTAAATGAGTTCACATTTCCTCGAATCCGTGGAACTGGCT 597
Qy 633 ggaactcattgcatggaaacagatcgcaactgttttccggcgacgaagcgaactc 692
Dy 598 GGACTTCAGTTCATTTACCTTGGCGTATGTGGGTGCAGCGATAGACCTCCGAGGAA---T 654
Qy 693 ttcagctcttgtaacctccagtggttcagagctctgaagcgatttcagttatctcagg 752
Dy 655 CTCAGGCGTCGGACATTCGAGTTCACAGAGCCCTGAAACTGTTCTGTGATCCCCAGG 714
Qy 753 tctgaagctcatgtagtgccttgcgtgcgtggaagaagctggttagacgtgatggt 812
Dy 715 ACTGAAGTTCATCGTGGAGCCCTGATCCACTCAGTGAGGAAGCTGGCCGACGTGACTAT 774
Qy 813 cctcaactctctgcctcagcatctttgcccctggctcagcagctgttctcaggaat 872
Dy 775 CCTCACAGCTCTTCGCTGAGCGCTTTCGCTTGGTGGCCCTGCGAGCTCTTTAAAGGGAA 834
Qy 873 tctgaacagagtgattaaagcaactgtggcccaaccctgcatccaac----- 924
Dy 835 CCTTAAGAACAAATGCTACGAAAGGACAGATCCCCACAGAGCTGACAACTCTCATC 894
Qy 925 -----aaggtatgctttgaaagggaaaaagatagcgaagacttcaatgtgtggtac 977

LPRLMTDQWENLFOJTLRAAKTYMIFPVVIFLGSFVLINLIILAVMAYAEQNEA
TLAEQKEEEFQMLEKFKHOEELEKAKAAOLEGGEADGDTPHSDKDCNGSLDTS
GKGPPRPSKSAESAIISAMEELEEHAQKPPWYKCKAKHVLIMWCCAPWFKHIL
LIVMDPFDVLTGTCIVLNTFLPAMEHYPMTEBFDNVLVSLVGLVFTGIFPAKSWPLKLI
ANDPYEYFOQGNIPDSFVTLISVELGLIANVQGLSVLRSLRLLVFKLAKBMTPLNI
LKIIIGNSVAGLNLTLVLIAIIVFANVVGKQLRFGKSKYECVCKTASDCSLRPHWHD
FPHSLFRIICGEMWETMDCMEVAGAMCLTVFLMWVJGNLVLNLFLLALLSG
FSADELADEGEMNNQIAIGRIKQWIAFAKTEFLGLLHGKILLSKDIMLSLGE
GAGENGESPEDEKPEPPEDGNKONHILNHVGLTDGPRSSIESIMHUNFINNPYL
TTHVLIASDEPLEMETETOTFSEPIDKKPLOPLYDGNSSVCSADYKPEDEPE
EOAENPEGELPEECFTEACVKRCPCLVVDISQGRGKMWTLRRACFKIVEINWETEF
IVPMILLSSGALAFEDILYEORVIRTILEYADKVFTYIFILEMLLKWYAGFKYVFT
NAWCMDFLIVDVSISLVANWLGISELGPISKRLRALRPLRLRSRVEGRVYVNA
LUGAIPSNMVLVCLLFWLIFESIMGNLFAKGYFCINTTSERPDISVWNKSECE
SMYTGGOVMNVKYNVDYGLISLQVATFKGMMDIYAAVDSREKEEOPDEYEVN
LYMYLIFYFIIIFGSPFTLNLFIIDNFNOQKRFKGGKIDFMTEQOKKYFNAMKLI
GSKKPKPIPRQNKIQGMVYDFVTQKQFEDISIMILICLNMVMTMAVETDDQSOLKVI
LYNINMFIIVTGEVLMKFAIRHYFTFIGNNIFDFVYVILSVGLALSILQIXFY
SPTLFRVIRIARIGRVLRIKAGIRTLULFALMMSLPALFNIGLILLFLVMFYISIFG
MNSFAYKKSIGIDMFNETFSGNISLICFEITTSAGWDGLNPLNLSGPPDCDPTLE
NPGTNIKGDGNPSIGICFPFSYIIISFLIVVMYIAIILEFNPNVATESSPPLACEDD
FMFVETWEKFPDPDATQFTDYSLRSDVDTLOEPLKIAKPNKIKLITLDPVWPGDKI
HCLDILFALTKEVLGDSGEMDALKOTMEKPMANPSKVSYPEITTLTKRKOEEVCAI
KTQRAYRHLLORSVQKQASMYRHSQBGNGDCAPKEGILLANTMKMKYSEKEDNGVO
SOGREKSDTEADGPTTEVTAPSSDALTTPPPSPPPPPPPQGTVRPGVKESLV*
BASE COUNT 1347 a 1680 c 1534 g 1326 t
ORIGIN

Query Match 23.8%; Score 1406.4; DB 10; Length 5887;
Best Local Similarity 57.1%; Pred. No. 0;
Matches 2998; Conservative 0; Mismatches 2121; Indels 129; Gaps 19;
QY 66 ccggtgatctcccgagagcggaattccgcccctcaactcgaactctctgctgc 125
DB 22 CACCTGGTCCCCCTGGTCCCCACTGCTCGCCCTTCCACCCAGAGTCCCTGGCAGC 81
QY 126 cataaagaagcgg---attgctatccaaaggagagaagaagtcacaaagaagcgc 182
DB 82 CATAGAACACGGGCAATGAGGAGGAAGCCGGCTGCACGGAAACAAGCAATGGAGAT 141
QY 183 agctgagccccagcctgagctcagcttgacctaaaggcctcaggaagttaactaagct 242
DB 142 TGAAGAGCCTTGAGCGGAAGCACGACGTGACCTGGAAGCTGGCAAGACCTCCACTCAT 201
QY 243 ttatggtgacattcccctgagctgttacgaaacctctgagagacctgagccctacta 302
DB 202 CTATGGGACCCCTCAAGTCATTTGGCGTCCCTCGAGGACCTGGACCCCTTACTA 261
QY 303 caaagaccataagacattcattggttgaaagaagaagaacatttatcgcttcagcgc 362
DB 262 CAGTGACAAGAAGACCTTCATTGTGCTCAACAAGGAAGGCCATCTTCCGATCTCTGC 321
QY 363 caagcgggcttgatcttcattcgggcttttaattccctcagagcttaattgattgat 422
DB 322 CACCCCTGCCCTCTACATGCTGAGCCCTTCAGCATGCTCGCGGGTGGCTATCAAGGT 381
QY 423 ctctgtccattcagcttttagcattgttcacatctgacggtgacatcaactgatgtt 482
DB 382 GCTCATCCAGCGGTGTTCAGCATGTTTCATGATCACCATTCTTGACCAACTGCGTGT 441
QY 483 catggcgaaattctatgagagaagtttcgacaacgacattcccgaaatcgtctctattg 542
DB 442 CATGACCATGACNAACCGCTTCTTGGTCCAAGGAGCT---GGAGTACACCTTCACAG 498
QY 543 gatttatatttagaagctgtagtaataattggcaagaggttcaattgtagatgatt 602
DB 499 GATCTACACCTTTGAGTCCCTCATTAAGATGCTGGCCCGGAGGCTTTTGCAATTGACTT 558
QY 603 ttccttccctcagagatccgtggacgtgctggacttcaattgatttggaacagcgtatgc 662
DB 559 CACATTCCCTCCGAGACCCCTGGAACCTGGCTGGACTTTCAGTGTATCATCAATGGCGTACGT 618

QY 663 aacttgttttccgggagcagcaagtcacttctcagctctctcgtacactctcagtggtcag 722
DB 619 GACAGAGTTTGTGG---ACTTGGGCAACATCTCAGCCCTGAGGACCTTCGCTGTCTGG 675
QY 723 agcttgaaggcgaatttcagttatcagttatcaggtctgaaggtcactgtaggtgcctgctg 782
DB 676 GGCCCTGAAAACCATCAGGTCATCCAGGGCTGAAGACGATCGTGGGAGCCCTGATCCA 735
QY 783 ctggttgaagaagctggttagacgtgattggttcctcactctcttctgctcagcacttctgc 842
DB 736 GTCTGTGAAAACCTCTCGGATGATGATCCTCACTGTCTTCTGCTGAGCGCTTTGC 795
QY 843 cctggttcagcagcgtgcttcaatggtgaaattctgaaccagaaagtatgatt---taagcaaa 899
DB 796 CTTGGTGGGCTGACGCTTTTCATGGGAAACCTGCGTTCAGAGTGGCTGCGTGGCCCC 855
QY 900 ctgtggccccacccctgcatacccaagattgctttgaaaggaagaaagatacgagaaga 959
DB 856 GCCCATGATGACCAACACACCGTGGTATGATGATGATGATGATGATGATGATGATGATGAT 915
QY 960 cttcaataatgtgtggtacctgctcgcagcagacccctgtcccaatggttctcagtcgca 1019
DB 916 CTGCTACGGCAATGACACCTGGTATGCAATGACACTTGGCAACAGCCAGGAGCTGGGT 975
QY 1020 taaaaccac-----attgaaccagacaataattatacaaaagtttgacaactt 1067
DB 976 CAGCAACTCTACCTTTGACTGGGAGGCTACATCAATGACGAAGGAACCTTCTATTCTT 1035
QY 1068 tggctggtctctcgcagatgttcggggttatgaactcaagactcctggagagaggttta 1127
DB 1036 GGAGGCTCCAAATGATGCCCCCTGCTGTGGGAATAGCAGTATGCGGGGACTGCCCCCTGA 1095
QY 1128 ccgacagatcctgagacccctggtggtacttctgttcttcttctgtgtggtggtcactt 1187
DB 1096 GGCTACGAATGATGAGGCTGGGAGGAACCCCAACTATATGCTACACACTACGACAC 1155
QY 1188 cctgggtcctcttactcgtcttaacctaacctggtgtgtgtcaccatggcttattgaaga 1247
DB 1156 CTTGAGCTGGGCTTCTGCTCTCTTCCGCTCTCATGACGACGAGTACTGGGAGAACCT 1215
QY 1248 acagaacagaaatgtagctctgagacagagggccaagagaaataatgtttcaggaagccc 1307
DB 1216 TTTCCAGCTACCCCTTGAGCTGCTGGCAAGACCTACATGATCTTCTTGTGTGTCATCAT 1275
QY 1308 gcagctgttaaggagagagagagcgtctggttgccatgggaatgacagagattccct 1367
DB 1276 CTTCTGGGTTCCTTCTACCTCATCAATCTGATCCTGGCGGTGGTGGCCATGGCATATGC 1335
QY 1368 taattccctcagcgttctccttttcccgagaagaggaagtgttttcggttagtaagac 1427
DB 1336 TGACGAGAATGAGCTTACCC---TGCGCGAAGACCCAGGAGAGAGGAGGATTCCAA 1390
QY 1428 aagaagtccttctttagagaggttccaaagcggcccaagcctcagcgtctgattcaga 1487
DB 1391 CAGATGCTTGAATAAATTCAAAAAACAATCAGGA---GGAACCTGGAAGAGGCGAGGTGCCCA 1449
QY 1488 ggaagatgctctcaaaatccacagctccttgagcagaccaaagcactgtccccagaactt 1547
DB 1450 GGCTCTGGAAGGTGGAGAGGAGCAGATGGGACCCCAACCCACAGCAAAAGACTGCAATGG 1509
QY 1548 gccagtggtatctcttgatgagcagcgtggaccctccacagagcagagagcgtgagcgc 1607
DB 1510 TAGCTGGATACATCCGGGAGAGGGGCCCCCAAGGCCAAG-----CTGCAGCGC 1560
QY 1608 tgcagtatcttaaccatcaccatacaggaacaaagaaaaattccagagagcctgtttcc 1667
DB 1561 AGAGAGTGCCTATCTCAGATGCTATGGAGGAGCTGGAAGAGGCCCATCAGAAAGTGCCTCC 1620
QY 1668 atgtgggaataattggcctcctgaatcctggtgtggagactgagcctcagtgagctgtg 1727
DB 1621 ATGTTGTACAAAGTGTGCACAAAGTGTCTCATCTGGAACCTGTGTCCTCCCGTGGGTGAA 1680
QY 1728 cataaagaaggtcctgcgaccatcatgacggtatcccttttactgagctggccatcaccat 1787

BASE COUNT 1542 a 1863 c 1663 g 1459 t

Query Match 23.8%; Score 1405.2; DB 6; Length 6527;
Best Local Similarity 57.5%; Pred. No. 0;
Matches 3246; Conservative 0; Mismatches 1923; Indels 477; Gaps 21;

Qy	45	gaagatggagagaggtactaccgcggtgatctctcccggaacgagcgaatttccgccttt	104
Db	191	GAAGAATGAGAAGATGGAGCTTCCCTTTGCGTCCGTGGAACTACCAATTTTCAGACGGTT	250
Qy	105	cacttcgactcttgctgctcataaagaacggatgctctaccaaagagagagaagaa	164
Db	251	CAC'TCCAGAGTCACTGGCAGAGATCGAAGACGATGTCTGCTCACCGGGCAGCAAGAA	310
Qy	165	gtccaaagacaagcgcgagctgagcccc-----agctcggcctcagctga	212
Db	311	GGCCAGAACCAAGCACAGAGGACAGGAGGACAAAGGCCAGAGCCAGGCCCTCAGCTGGA	370
Qy	213	octaaagcctccaggaagtaccataagctttatggtgacattccccctgagctgttac	272
Db	371	CTTGAAGACTGTAACAGCTGCCAAGTTCTATGTTGAGCTCCACAGCAGAACTGGTCGG	430
Qy	273	gaaccttgagagacctggacccctactacaaagacacataagaacattcatggtgtgaa	332
Db	431	GGAGCCCTGGAGACCTTAGACCTTTCTACAGCACACACCGCGACATTTCATGTTGTA	490
Qy	333	caagaaagaacaattatcgcttcacgcgccaagcgccctgttctatctgggcccctt	392
Db	491	TAAAGCAGGACCATTTCCAGATTCAGTGCACCTTGGGCCCTTGGGCTCTTCAGTCCCTT	550
Qy	393	taatccccagagacttaattgattcgctatctctgtccattcagctctttagcattgtcat	452
Db	551	CAACTGATCAGAAAGACAGCCATCAAAAGTGCTGTCCATTCTCTGTTTCCATATTCAT	610
Qy	453	catctgacggtgatcatcaactgatgttcattgctggaattctatgagagaagttcga	512
Db	611	CACCATCACTATTTTGTTCAACTGCGTGTGATGACCC-----GAACGTGATCT	658
Qy	513	caagcattccccgaatacgtcttcattggtatttatatttaagaagctggtgataaat	572
Db	659	TCCAGAGAAAGTCGAGTACGCTTCACATGTCATTACACCTTCGAGGCTCGATTAGAT	718
Qy	573	attggcaagaggtctcatgttgatgagtttctctcccgagatccgtggaaactggct	632
Db	719	ACTGGCAGAGGGTTTGTCTAAATGAGTTCACATTCTTCAGATCCGTGGAACTGGCT	778
Qy	633	ggacttcattgtcattggaaacgagatgcgaactgttttccggcgacgaagccaatcct	692
Db	779	GGACTTCAGTGTCAATTACCTTGGCGTATGTGGGTGCAGCGATAGACCTCCCGAGGAA--T	835
Qy	693	ttcagctcttgtaacctccagtggttcaagagctctgaagcgatcttcagttatctcagg	752
Db	836	CTCAGGCCCTCGGACATTCGGAGTTCACAGAGCCCTGAAAACCTGTTTTGTGTGATCCCAGG	895
Qy	753	tctgaaggtcatgtaggtgccttgctgcgctcggtagaagcgtgttagacgtgatggt	812
Db	896	ACTGAAGGTCACTGTGGGAGCCCTGATCCACTAGTGAGGAAGCTGGCCGACGTGACTAT	955
Qy	813	octcactctctctgcctcagcatcttttgcctggtgcggtcagcagctgttcatcaggaaat	872
Db	956	CCTCACAGTCTCTCGCTGAGCGCTTCGCGCTTGGTGGCCCTGCAGCTCTTTTAAGGGAA	1015
Qy	873	tctgaaccagaagtgtattaaagacaactgtggccccaaacctgcataccaac-----	924
Db	1016	CTTTAAGAACAATATGCATCAGGAACGGAACAGATCCCCACAGGCTGCACAACTCTCATC	1075

QY	925	-----aagattgctttgaaaggaataagacagcaagactctcataatgtgtggtac	977
Db	1076	TGAAATGGCAGAAATACATCTTCATCAAGCCTGGTACTACGGATCCCTTACTGTGCGGCAA	1135
QY	978	ctggctcggcagcagaccctgtcccaatggttctacgtgcgataaaaaaccacattgaacc	1037
Db	1136	TGGGTCTGATGCTGGTACATGCGCTCGAGGCCTATGCTGCTGCTGAAACATCTCTGCAACCC	1195
QY	1038	agacaataatatacaaagttagacaactttggctgggtccctttctcgcatgttccgggt	1097
Db	1196	GGATTTTAACATACACCAGCTTGATTCCTTTGGTGGGATTCCTCTCACTGTTCCCGCT	1255
QY	1098	tatgactcaagactcctcgggagaggctttaccgcagagatcctcggacctctgggacta	1157
Db	1256	CATGACGAGACTCTCTGGAGCGCTGTACACGACAGACACTCGGGCTTCTGGGAAAT	1315
QY	1158	cttgctcttcttctgggtgggtcattctctcgtggctcctctcactgcttaacctaac	1217
Db	1316	GTACATGGCTTTTTCGTGCTGTTATTTTCTTGATGCTTCTACCTGGTCAATTTGAT	1375
QY	1218	cctggctgtgtcaccatgcttatagaagaacagaaacagaaatgtagctcgtgagacaga	1277
Db	1376	CTTGGCGTGGTCACCATGCGGTATGAAGAGCAGACCAGGCACAAATTCAGAAATCGA	1435
QY	1278	ggccaagagaaaaatgtttcagaaagcccgacgtgttaaaggaggagaaaggagctct	1337
Db	1436	AGCCAAGGMAAAAAGTTCCAGGAAGCCCTTGAGGTGTGCAGAAAGAACAGGAGGTCT	1495
QY	1338	ggttgcacatgggaattgaacagaagttcccttaattccctcgaagctcactcctttccc	1397
Db	1496	GGCAGCCCTGGGATTTGACACGACCTCGCTCCAGTCCCATCCACAGTGTATCACCCTTAGCCTC	1555
QY	1398	gaagaa-----gaggaagttttcgtagtgaagacaaagaaagtccttcttatgaga	1449
Db	1556	CAAAACGCCAATGAGAGAAGACCCAGGGTGAATCAAGGGTGTGAGAGGGCTCCACGGA	1615
QY	1450	gggtccaagacggcccaagcctcagcgtctgtatccagagacgatgcctctaaaaatcca	1509
Db	1616	TGACAACAGGTCAACCCCAATCTGACCCCTTACAACACAGCGCAGGATGCTTTCTTAGGCTC	1675
QY	1510	cagctccttga-----gcagaccaaacagactctccacagaacttgcca	1551
Db	1676	GTCTTTCAGGAAGACGCGAGGCTTAGCCACGGCAGTGTGTTTCCACTTCCGAGGCGCCAGCCA	1735
QY	1552	gtgactcttt-----gtgactcttt-----	1562
Db	1736	AGACATCTCATTTCTTGACGGGATACCCCTGATGATGGGGTCTTTCACGGAGACCAAGGA	1795
QY	1563	-----tgatgagcagctggagccctccacag	1589
Db	1796	AAGCGTCGAGGTTCCATATTGCTGGCAGGGGTGCTGGGCAGACAGGTCCACTCCCCAG	1855
QY	1590	g-----	1590
Db	1856	GAGCCCACTGCTCAGTCCCCCAACCCCTGGCCGTAGACATGGAGAAGAGGGACAGCTCGG	1915
QY	1591	-----	1590
Db	1916	AGTCCCACTGGTGAGCTTACCCTGGAGCGCTTGAAGCCCGGCACCTCGACACTACAGG	1975
QY	1591	-----cagagagcgt	1601
Db	1976	CGAAGAGGCTTCTGCTCGGGCTACTTGAACGNAACCTTTCGAGCAGCAGAGGGCCAT	2035
QY	1602	gagcgtgtcagtatcttaaccatacaccatacagaaacaagaaaaattcccaggagccttg	1661
Db	2036	GAGCGTTGTCAGTATCATGACTTCTGTCAATTGAGGAGCTTGAAGAGTCTAAGCTGAAGTG	2095
QY	1662	tttcccatgtgggaaaaatttggcctctcaagtacctgtgtgtgggactgaacctcagtg	1721
Db	2096	CCCACCTGCTGATCAGCTTCGCTCAGAAGTATCTGATCTGGGAGTCTGCTCCCAAGTG	2155

Qy	1722	gctgtgataaagaagttcctgcgacacatcatgacgcatccctttactgagctgcccac	1781
Db	2156	GAGGAAGTTCAAGATGGCGCTGTTCAGCTGGTGAATCTGACCCCTTCGCAGAGCTTACCAT	2215
Qy	1782	cacactcgcacatcatcaatcacggtttcttaacgctggagacacacaacatgcatga	1841
Db	2216	CACCCTCTGCATCGTGGTGAACACCGCTTCATGCCCATGGAGACACTACCCCATGACCGGA	2275
Qy	1842	caacttaagacacactactgaaataggaaactgggttttcacgggaaattttcatagcga	1901
Db	2276	TGCCTTCGATGCCATGCTTCAAGCCGGCAACATTGCTCTACCGTGTGTTTTTCACAATGGA	2335
Qy	1902	aatgtgtctcaagatcatcgcgctgcgcaccccttaccactactctccggcgcagctggaatgt	1961
Db	2336	GATGGCCTTCAAGATCATTTGCCCTTCACCCCTACTATTACTTCCAGAAGAAGTGGAAATAT	2395
Qy	1962	ttttgacagcatcgtggccctcctgagtcgatgtgctctacaacacactgctcga	2021
Db	2396	CTTCGCATGTGTCTCATCGTCACCGTAGCCCTCTCGAGGTG-----AGTGCATCCCAAGAA	2449
Qy	2022	taacaaataggctttcttggtctccctcagagtcgtgaggtctctcaagttagcacaactc	2081
Db	2450	GGGACGCTCTCTGTGCTCCGTTCCTTACGCTTGTCTCGGGTCTTCAAGCTGGCCAAATC	2509
Qy	2082	ctggcccaacttaaacactctcattaagaatcctggccactccctgggcgcgtgtggaaa	2141
Db	2510	CTGGCCCAACCCTGAACACCCCTCATCAAGATCATCGGAACCTCAGTGGGGGCCCTGGGCAA	2569
Qy	2142	cctgactgtgctcgaactatcgtggtcttcactttcttgtgtgtggcgcagctgcctct	2201
Db	2570	CCTGACCTTTATCCTGGCCATCATGCTCTTCATCTTCGCCCTGTGCGAAGACAGCTTCT	2629
Qy	2202	c-----ggcaccaagttaaacagaccctcaecgccaccagagcgcgccagcgcgcg	2255
Db	2630	CTCAGAGGACTACGGGTGCCGAAGCAGGCGCTCTCCGTGTGGAACGCGGAGAGACTCCG	2689
Qy	2256	ctggcacatggataattctaacactcctctcgtgtgtgttcocgcatacctctgtgggga	2315
Db	2690	CTGSCACATGTGTACTTCTTCATTCCTTCCTGTCTCTCGAATCCCTCTCGGGGA	2749
Qy	2316	atggatagaacatgtgggctgcacatcagagatgagcagcgtcccgcttgatcatcat	2375
Db	2750	GTGGATCGAAGACATGTGGTCTGTCATGAGGTGACGACAGCAAAATCC---ATCTGCCCTCAT	2806
Qy	2376	tgtctttgtcctgataatggtgatcgggaagcttgtgtgtctaaacctcttcactgcctt	2435
Db	2807	CCCTCTTCTGACTGTATGGTGTGGCAACCTAGTGGTGTCTCAACCTTTTCATCGCTTT	2866
Qy	2436	gctgctcaattctctcagcaaatgagagagagatgggagcctggaagagagacacagaaa	2495
Db	2867	ACTGCTGAATCTCTCAGCGCGGACAAACCTCACGGCTCCAGAGATGACGGGAGGTGAA	2926
Qy	2496	aa-----ccaaagtgcagctagcctggatcgggttccgcgcgggcctt	2537
Db	2927	CAACTTGCATTTAGCACTGGCCAGGATCCAGGTACTTGGCCATCGGGCCAGCAGGGCCAT	2986
Qy	2538	ctccttcactgtcgcgctcttcagagtttttgttgcagaag-----	2579
Db	2987	CGCCAGTTACATCAGCAGCCTATGCCGATTCCTCGCTGGCCCAAGGTGGAGACCCAGCTGGG	3046
Qy	2580	-----atgcaggaggaanaactcgcgaagcccaaaaagacacacagaagactt	2627
Db	3047	CATGAAGCCCCACTACCAAGCTCAGAGGCCAAGAACACATTTGCCACTGATGCTGTCTAG	3106
Qy	2628	tgctgttgagaataaagactcaatcctccggatcgcaggcccttggaaggatgatcatc	2687
Db	3107	TGCTGTAGTGGGAACCTGACAAAGCCAGCTCTCAGTAGCCCCCAAGGAGAATCATCGGGGA	3166
Qy	2688	agacatggctttgtacacttgacagcgcggggtccgcgtgg-----ccccact	2735
Db	3167	CTTATCATCTGATCCCAACGTGTGGGTCTCTGTGCCCATTTGCTGAGGGGGGAATCTGACCT	3226
Qy	2736	cgcagaggttagagacgatgtgaaatttgt-----ggtgagcgcgcgtgccc	2781

db	3227	CGACGAGCTCGAGGAAGATATGGACGAGGCTTCGCAGAGCTCTCGGAGGAAGAGGACCC	3286
Qy	2782	ctaccacacctcaacaatagtgctggagttcaagccggtgacctccctccagagaccaa	2841
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SCN4A gene; skeletal muscle sodium channel.
KEYWORDS
Norway rat.
SOURCE
Rattus norvegicus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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1 (bases 1 to 5523)
Diss,J.K., Stewart,D., Fraser,S.P., Black,J.A., Dib-Hajj,S., Waxman,S.G., Archer,S.N. and Djamgoz,M.B.
Expression of skeletal muscle-type voltage-gated Na+ channel in rat and human prostate cancer cell lines
FEBS Lett. 427 (1), 5-10 (1998)
JOURNAL
MEDLINE
98273645
REFERENCE
2 (bases 1 to 5523)
Archer, S.N.
Direct Submission
Submitted (21-APR-1998) S.N. Archer, International Marine Centre, Localita sa Mardini, 09072 Torregrande, Oristano, ITALY
JOURNAL
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Best Local Similarity 57.1%; Pred. No. 0;
Matches 2995; Conservative 0; Mismatches 2116; Indels 132; Gaps 19;

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DR P-PSDB; AAY41668.

XX Mammalian sodium channel protein for treating pain and hypersensitivity
PT Claim 4; Page 52-58; 73pp; English.
PS The present sequence encodes rat sensory neuron specific 2a (SNS-2a).
XX SNS-2a is a sodium channel protein. SNS-2a can be used in a method for
CC the identification of a modulator of a sodium channel, and for assaying
CC for compounds which modulate sodium flux. The sodium channel modulators
CC can be used in a medicament for the treatment of pain or
CC hypersensitivity.
XX
SQ Sequence 5897 BP; 1474 A; 1471 C; 1435 G; 1517 T; 0 Other;

Query Match		100.0%;	Score 5897;	DB 20;	Length 5897;
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DE	XX	Rat sodium channel NaN cDNA.
XX	XX	Sodium channel; NaN; rat; tetrodotoxin resistant; pain;
KW	XX	paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
KW	XX	diagnosis. ss.
XX	XX	
QS	XX	Rattus norvegicus.
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Db	5709	ctgccacatgtagctcttttttgatgtacgttcaaaacccctgcagtaagtttaataagcttg	5768

QY	5739	ctacggggtgttctaccagcatcacagaaattgggtggtatgactcaaacctaaagcatga	5798
Db	5769	ctacggggtgttctaccagcatcacagaaattgggtggtatgactcaaacctaaagcatga	5828
QY	5799	ctctgacttgtcagtcagcacccgacttcagacgctcccaatctctgtgccagggtctct	5858
Db	5829	ctctgacttgtcagtcagcacccgacttcagacgctcccaatctctgtgccagggtctct	5888
QY	5859	aacgaataaatagggtaaaag	5878
Db	5889	aacgaataaatagggtaaaag	5908

RESULT 4

AAx87600
ID AAx87600 standard: cDNA: 5875 bp.

XX
AC AAX87600:

XX
DT 26-OCT-1999 (first entry)

XX DE Rat sodium channel Nan cDNA.

XX	
KW	NaN: sodium channel: ion transport: rat: dorsal root ganglia:

NAN; sodium channel; ion transport; rat; dorsal root ganglia;
KW pain; paraesthesia; hyperexcitability; therapy; scnlla gene; ss.

XX OS Rattus sp.

XX	Key	Location/Qualifiers
FH		

EH	Key	Location/
ET	CDS	41..5338

FI
FT
CDS
41.13338
/*taq= a

```
FI      /-cay- a
FT      5551.: 560
        misc_feature
```

```
FT      misc_recurve      33311..3300
FT      /*tag= b
```

FT "these bases represent nucleotides missing from the sequence given in Fig 1 of the specification. The nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

XX PN WO9938889-A2.

XX
PD
05-AUG-1999.

FD 03-AUG-1999.
XX

PF 29-JAN-1999; 99WO-US02008.

XX
11
0007050 0066 1555 0000 02

PR 20-NOV-1998; 98US-0109402.

PR 29-JAN-1998; 98US-0072990.

XX

PA (UYYA) UNIV YALE.

XX

PI D1b-Hajj S, Waxman S;

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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that express Na_v, methods for identifying agents that modulate Na_v channel activity or Na_v channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of Na_v in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The Na_v gene has been named Scn11a.

Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 52 other;

Query Match

Best Query Match	98.4%;	Score 3803.8;	DB 20;	Length 3873;
Best Local Similarity	98.9%;	Pred. No. 0;		

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... Best Local Similarity 98.9%; Fied: NO: 0;
... Matches 5811: Conservative 0: Mismatch
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9 acggtaccctgattcctctgtaccaggaagacagaggttgaagattgagaggaaggtactacc 68

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Qy	3069	ccacaaacagacaagagaaagtcocccctgggtcctgtggtggaacattcggaaaaacctg	3128
Db	3061	ccacaaacagacaagagaaagtcocccctgggtcctgtggtggaacattcggaaaaacctg	3120
Qy	3129	ctaccaaaatcgtaaacacacagctgggttgagagtttcaatactttgtattctgtcgag	3188
Db	3121	ctaccaaaatcgtaaacacacagctgggttgagagtttcaatactttgtattctgtcgag	3180
Qy	3189	cagtggagcgtgatatttgaagatgtcaattcccccagcggcccaagtgtgagaatt	3248
Db	3181	cagtggagcgtgatatttgaagatgtcaattcccccagcggcccaagtgtgagaatt	3240
Qy	3249	actaaggtgtacggataataatttcaacatttattttccctcgaaatgatctcgaagt	3308
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Qy	3309	ggctggccttggattccggaggtatttcaccagtgctgtgctggcttgaatttcctcat	3368
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Qy	3609	cgggacagacataaatagtatttgagttttaccgaagtcgcgaacccgaagccaattgaa	3668
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Qy	3789	cgattccagagagaagacagcagccgagctttgagcgaacctctacgcgtatctcta	3848
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Db	4201	catctttaccatagatgtctcatcaaaagtctttgtctttgagcgacactacttcaccaa	4260
Qy	4269	tggctggaaactatttgattgtgtgctgctggtttcttctatcatctagctcgtgtttc	4328
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Qy	4329	cgcgttgagagacagtgaactttcttcccgcccacgtctcttcagagtcgttcgcgttggc	4388
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Qy	4389	tcggaattggtcgaactctcaggctggtccgggctgcgcgggaaatcaggacacctctct	4448
Db	4381	tcggaattggtcgaactctcaggctggtccgggctgcgcgggaaatcaggacacctctct	4440
Qy	4449	tgctttgatgatgtctctcccctctctctcaaacatcgcttgcctgctcttcttcgtgtgat	4508
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Db	4801	caacacagccagggagagcgagagaccctctgggagagcagcactttgaaattctcta	4860
Qy	4869	tgaggtctgggagaagatttgaccccgaggcgtcgcagttctatccagtatctcgccctctc	4928
Db	4861	tgaggtctgggagaagatttgaccccgaggcgtcgcagttctatccagtatctcgccctctc	4920
Qy	4929	tgaactttcggagacgccttcggagaccgttgcggttgcccagacggaataagtcttcagtt	4988
Db	4921	tgaactttcggagacgccttcggagaccgttgcggttgcccagacggaataagtcttcagtt	4980
Qy	4989	tctagtgtgacttgcccatggtgatgggcagcgcctcccattgcattgagttgctctct	5048
Db	4981	tctagtgtgacttgcccatggtgatgggcagcgcctcccattgcattgagttgctctct	5040
Qy	5049	tgctttcactaccaggttctctcgggaactccagcggtctgggataccatgaaacacatgat	5108
Db	5041	tgctttcactaccaggttctctcgggaactccagcggtctgggataccatgaaacacatgat	5100
Qy	5109	ggagagaagtttatggaggccaaaccccttttaagaagctctctacgagcccatagtcaccac	5168
Db	5101	ggagagaagtttatggaggccaaaccccttttaagaagctctctacgagcccatagtcaccac	5160
Qy	5169	caccaagaggaagagagagcaaggcgcgcctgtcatccagaggggctactacggaaaaa	5228
Db	5161	caccaagaggaagagagagcaaggcgcgcctgtcatccagaggggctactacggaaaaa	5220
Qy	5229	catgagagaagtgttcaaaactgagactgaagagacaggtcaaatctcatctcaccaggtgt	5288

|||||
Db 5221 catggagaagatgtaaaactgagctgaagcaggtcaagttcatcgaccaggtgtt 5280
QY 5289 ttgcaatggagactgtccagcttgatgtgccaaggtcaaggttcaaatgactgaac 5348
Db 5281 ttgcaatggagactgtccagcttgatgtgccaaggtcaaggttcaaatgactgaac 5340
QY 5349 cctcatctccaccctacactcactgcctcagcttagctccagctctggcgagcagg 5408
Db 5341 cctcatctccaccctacactcactgcctcagcttagctccagctctggcgagcagg 5400
QY 5409 cggcagactcactgaacacacagcgcttcgactgtgttttggctgaacagagtgacagg 5468
Db 5401 cggcagactcactgaacacacagcgcttcgactgtgttttggctgaacagagtgacagg 5460
QY 5469 ttggcgtccatttttaaatgactcttggaagatttcattatgagagatgttagaaggga 5528
Db 5461 ttggcgtccatttttaaatgactcttggaagatttcattatgagagatgttagaaggga 5520
QY 5529 ctgcaaaaggacacgaccataacggaagcgctggaggacagtcacacttataaagatg 5588
Db 5521 ctgcaaaaggacacgaccataacggaagcgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 5580
QY 5589 agaaacaagaaggaagatcccaggaaaacttcagattgttctcagtgatattcccca 5648
Db 5581 nnn 5640
QY 5649 tgtgtctgttcggtgttttggatgtgacctgacctgacctgacctgtcttttttgcagtac 5708
Db 5641 tgtgtctgttcggtgttttggatgtgacctgacctgacctgacctgtcttttttgcagtac 5700
QY 5709 gtcaaaacctgcagtaagtaagtctgtctacgggtgttctaccagcatcacagaat 5768
Db 5701 gtcaaaacctgcagtaagtaagtctgtctacgggtgttctaccagcatcacagaat 5760
QY 5769 tgggtgtatgactcaaacctaaagcatgactctgacttgcagtcagcaccgcgacttt 5828
Db 5761 tgggtgtatgactcaaacctaaagcatgactctgacttgcagtcagcaccgcgacttt 5820
QY 5829 cagacgtccaactctctgtcccagggtgtctaagcaataaataaggttaaaagaaaaa 5883
Db 5821 cagacgtccaactctctgtcccagggtgtctaagcaataaataaggttaaaagaaaaa 5875

RESULT 5
AAX60244
ID AAX60244 standard; cDNA; 5334 BP.
XX
AC AAX60244;
XX
DT 11-AUG-1999 (first entry)
XX
DE Stabilised cDNA encoding type 5 sodium channel protein designated PNS.
XX
KW Type 5 sodium channel; PNS; nervous system; plexiform;
KW dorsal root ganglia; tetradotoxin; TTX; epilepsy; stroke;
KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
KW neuropathic pain; migraine; headache; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN FR2771103-A1.
XX
XX 21-MAY-1999.
XX
XX 19-NOV-1998; 98FR-0014551.
XX
XX 20-NOV-1997; 97US-0066225.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;

XX
DR
XX
PT Isolated DNA encoding sodium channel of the nervous system
XX
PS Example 7; Fig 5A-E; 90pp; French.
XX
CC The present sequence encodes a type 5 sodium channel protein
CC designated PNS. The protein is a sodium ion channel of the
CC nervous system, and is highly expressed in plexiform and dorsal
CC root ganglia. The protein can be used to identify inhibitors of
CC sodium channel proteins that are resistant to tetrodotoxin (TTX).
CC The inhibitors are potentially useful for treating epilepsy,
CC stroke, diabetic neuropathy, traumatic injuries, AIDS-related
CC neuropathy, and especially neuropathic pain, e.g. migraine and
CC headache.
XX
SQ Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 other;

Query Match 89.8%; Score 5295.6; DB 20; Length 5334;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 5304; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 39 cagggtgaagatgagagaggtactaccggtgactctccggacgagcggaatttcg 98
Db 14 cagggtgaagatgagagaggtactaccggtgactctccggacgagcggaatttcg 73
QY 99 ccccttcacttcgactctctgctgcataaaagaagcgatgtctatccaaaaggagag 158
Db 74 ccccttcacttcgactctctgctgcataagaagcgatgtctatccaaaaggagag 133
QY 159 gaagaagtcctcaaaagacagcgccagctgagcccgagcctcggcctcagcttgacctaa 218
Db 134 gaagaagtcctcaaaagacagcgccagctgagcccgagcctcggcctcagcttgacctaa 193
QY 219 ggcctccagaagttacctaaagctttatgtgacattcccccagctgtttacgaacc 278
Db 194 ggcctccagaagttacctaaagctttatgtgacattcccccagctgtttacgaacc 253
QY 279 tctggagagccttgacccttactacaaagaccaaaagacattcatgtgttgaacaagaa 338
Db 254 tctggagagccttgacccttactacaaagaccaaaagacattcatgtgttgaacaagaa 313
QY 339 aagaacaatttatcgcttcagcgccagcgccgtgtgttcatcttggggccttttaacc 398
Db 314 gagaacaatttatcgcttcagcgccagcgccgtgtgttcatcttggggccttttaacc 373
QY 399 cctcagaagcttaagtattcgtatctctgtccattcagctttagcatgttcatcatctg 458
Db 374 cctcagaagcttaagtattcgtatctctgtccattcagctttagcatgttcatcatctg 433
QY 459 cagcgtgatatcaactgtatttcatggcgaaattctatgagagaagtttcgacaacga 518
Db 434 cagcgtgatatcaactgtatttcatggcgaaattctatgagagaagtttcgacaacga 493
QY 519 cattcccgatacgtcttcattgggatttatattttagaagctgtgattaaaaatatggc 578
Db 494 cattcccgatacgtcttcattgggatttatattttagaagctgtgattaaaaatatggc 553
QY 579 aagaggcttcattgtgagatgattttctctcccgagatccgtggagctggcgactt 638
Db 554 aagaggcttcattgtgagatgattttctctcccgagatccgtggagctggcgactt 613
QY 639 cattgtcatttgaacacgcatcgaactgttttccggcgagccaaagtcactatcttcagc 698
Db 614 cattgtcatttgaacacgcatcgaactgttttccggcgagccaaagtcactatcttcagc 673
QY 699 tcttcgtacattccagatgttcagagctctgaagcgcatcttcagttatctcaggtctgaa 758
Db 674 tcttcgtacattccagatgttcagagctctgaagcgcatcttcagttatctcaggtctgaa 733
QY 759 ggtcactgtaggtgcacctgctggcctcggtgaagaagctggtgacgtgtagctggtcctcac 818

Db 5114 taagaagctctacagcccatgctaccaccaccacaaagaggaaggagaggaagcagcgc 5173
 Qy 5199 cgcgctcatccagagggcctaccggaacacacatggagaagatgggtcaaaactgaggtcgaa 5258
 Db 5174 cgcgctcatccagagggcctaccggaacacacatggagaagatgggtcaaaactgaggtcgaa 5233
 Qy 5259 gacaggtcaagtctatccacacaggtgtttgcaatgagagactgtccagcttgatgt 5318
 Db 5234 gacaggtcaagtctatccacacaggtgtttgcaatgagagactgtccagcttgatgt 5293
 Qy 5319 gqccaaggtcaaggttcacaatgactgaacctcatct 5356
 Db 5294 gqccaaggtcaaggttcacaatgactgaacctcatct 5331

RESULT 6

AAF30103

ID AAF30103 standard; cDNA; 5822 BP.

XX AC AAF30103;

XX DT 30-APR-2001 (first entry)

XX DE Mouse sodium channel NaN cDNA.

XX KW Sodium channel; NaN; Scn1a; mouse; tetrodotoxin resistant; pain;
 KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
 KW diagnosis; ss.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 XX CDS 19..5316

XX FT polyA_signal

XX FT polyA_site

XX FT WO200105831-A1.

XX PD 25-JAN-2001.

XX PF 14-JUL-2000; 2000WO-US19342.

XX PR 16-JUL-1999; 99US-0354147.

XX PA (UYVA) UNIV YALE.

XX PI Dib-Hajj S, Waxman SG;

XX DR WPI: 2001-103147/11.

XX DR P-PSDB; AAB20124.

XX PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium

XX PT channels, useful for preventing, diagnosing and treating pain,

XX PT paraesthesia and/or hyperexcitability phenomena .

XX PS Example 3; Fig 7A; 162pp; English.

XX CC The present sequence is that of cDNA encoding a novel mouse

XX CC tetrodotoxin resistant sodium channel, termed NaN (see AAB20124).

XX CC The cDNA was isolated from trigeminal ganglia cDNA using primers

XX CC (see AAF30102-21) based on rat NaN sequences. Mouse NaN shows

XX CC 68% similarity to human NaN (see AAB20121). The gene encoding NaN,

XX CC termed Scn1a, is located on mouse chromosome 9. NaN belongs to the

XX CC a-subunit voltage-gated sodium channel protein family and produces

XX CC a TTX-R sodium current. Such channels underlie the generation and

XX CC propagation of impulses in excitable cells such as neurons and

XX CC muscle fibres. Preferential expression of NaN on sensory neurons

XX CC innervating the body (dorsal root ganglia) and the face (trigeminal

XX CC ganglia), but not on other neurons, makes it a very useful target

CC for diagnostic and/or therapeutic uses in relation to acute and/or
 CC chronic pain pathologies. A claimed method of treating pain,
 CC paraesthesia and/or hyperexcitability phenomena in a human or animal
 CC subject involves administering an agent that alters sodium current
 CC flow through NaN channels, or which modulates transcription or
 CC translation of NaN mRNA, in dorsal root ganglia or trigeminal
 CC neurons. NaN nucleic acids are used in gene therapy to correct
 CC disorders associated with decreased sodium channel expression or
 CC (antisense) to down-regulate NaN expression, in the diagnosis of
 CC disease, and in the recombinant production of NaN polypeptides.
 XX
 SQ Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 1 other;

Query Match

Best Local Similarity 78.6%; Score 4633.8; DB 22; Length 5822;
 Matches 5193; Conservative 0; Mismatches 603; Indels 78; Gaps 12;

Qy 40 agggtagaagatggagagaggtactaccgggtgattctcccgacagagcggaatttcgcg 99
 Db 10 agggtagaagatggagagaggtactaccgggtgattctcccgacagagcggaatttcgcg 69

Qy 100 ccttcacattccgactctctgctgccataaagaagcgattctccaaaaaggagag 159
 Db 70 ccttcacattccgactctctgctgccataaagaagcgattctccaaaaaggagag 129

Qy 160 aagaatccaaagacagcgccagctgagccccagcctcgctcagcttgacctaaag 219
 Db 130 aagaatccaaagacagcgccagctgagccccagcctcgctcagcttgacctaaag 189

Qy 220 gctccaggaagttaaccttaagctttatggtgacattccccctgagcttgttacgaaacct 279
 Db 190 gctccaggaagttaaccttaagctttatggtgacattccccctgagcttgttacgaaacct 249

Qy 280 ctggaggaactggaccctactacaagaaccataagaacattcatggttgtaacaagaaa 339
 Db 250 ctggaggaactggaccctactacaagaaccataagaacattcatggttgtaacaagaaa 309

Qy 340 aagaacatttatcgcttcagcgccagcgccctgttctcattctggggccttttaacc 399
 Db 310 aagaacatttatcgcttcagcgccagcgccctgttctcattctggggccttttaacc 369

Qy 400 ctcaagaagcttaagtattcgttatctctgcttcattcagttttagcttgcattctgc 459
 Db 370 atcagaagcttcatgattcgtcattctctcattcagttttagcttgcattctgc 429

Qy 460 acggtgatcatcaactgattgttcatgaggaa-----ttctatggagagaatttcgac 513
 Db 430 acggtgatcatcaactgattgttcatgaggaa-----ttctatggagagaatttcgac 489

Qy 514 aacgacattcccgaaatacgtcttcattggatttatatttagaagctgtgataaata 573
 Db 490 agtaacattcccgaaatacgtcttcattggatttatatttagaagctgtgataaata 549

Qy 574 ttggcagaaggttcatgttggaatgattttctctcctcgcagatccgtggaaactggctg 633
 Db 550 ttggcagaaggttcatgttggaatgattttctcctcgcagatccgtggaaactggctg 609

Qy 634 gacttcattgtcattggaaacagcgatcgaaactgttttccgggagcgaagtc---aat 690
 Db 610 gacttcattgtcattggaaacagcgatcgaaactgttttccgggagcgaagtc---aat 669

Qy 691 cttcagctcttcgtaccctccagtggttcagagctctgaagcggtatttcagttatctca 750
 Db 670 cttcagctcttcgtaccctccagtggttcagagctctgaagcggtatttcagttatctca 729

Qy 751 ggctgaaggttcattcgtggtccctcgtcgtcgttggaagagctggtagcgtgatg 810
 Db 730 ggctgaaggttcattcgtggtccctcgtcgtcgttggaagagctggtagcgtgatg 789

Qy 811 gtctcactctcttctgctcagcatctttgcccctggctcagcagctgttcacatggga 870
 Db 790 gtctcactctcttctgctcagcatctttgcccctggctcagcagctgttcacatggga 849


```

QY 5251 aggtgaagacaggtcaagtccatgcaccaggtgttttgcattgagactgttcagc 5310
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5221 aagctgaagacaggtcaagtccatgcaccaggtgttttgcattgagactgttcagc 5280
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5311 ttgattgtgccaaggtcaaggttcacaatgactg-aacctcatctccaccctacctc 5369
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5281 ttgattgtgccaaggtcaaggttcattgtgactgaacccccacacctgcaagcctacctc 5340
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   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5341 acagctcacagcttagcctcagcctctggtgagagcagcggcagactcaactgaacag 5398
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5430 gccgttcgactgtgttttggctgaacaggtgacaggttgctgctccatttttaata 5489
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5399 gccgttcgactgtgttttggctgaacaggtgacaggttgctgctccatttttaata 5458
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5490 ctttggaaagatttcattgtagagagattgtagaaggactgcaaaaggacacacgcacata 5549
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5459 ttcttgaaagattgaactgcgaacatgttagaaggactgcaaaaggacacacgcacata 5518
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QY 5550 acggaaggcctggagacagctcacaattacataaagatgagaacaaagaaagatcc 5609
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5519 acggaaggcctggagacagctcacaattacataaagatgagaacaaagaaagatcc 5573
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5610 caggaaaacttcagattgtgtctcagtagatctcccaatgtgtctggtgttttga 5669
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5574 catg-----ctgttcagttttaa 5592
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QY 5670 gtatgacctgcacatgactgtcttttttgcattgac-----gtcaaaacccctgcag 5723
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Db 5593 gtatgacctgcacatgactgtcttttttgcattgac-----gtcaaaacccctgcag 5652
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5724 taagttaataagc-ttctcaggggtgtctaccagcaccacagaaattgggtgtatgactc 5782
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5653 taagtaataagc-ttctcaggggtgtctaccagcaccacagaaattgggtgtatgactc 5712
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5783 aaacctaaagatgactgtcagctgtcagcagcccgacttcacagcgtccaalc 5842
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5713 aaacctaaagatgactgtcagctgtcagcagcccgacttcacagcgtccaalc 5768
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5843 tctgtccagggtgtctaaagataaataagtgataaagataaagataaagataaagataa 5896
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5769 tctgtcctagggtgttgagacaaataaataaataaataaataaataaataaataaataa 5822
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```

RESULT 7

AAx87601
ID AAX87601 standard; cDNA; 5822 BP.

AC AAX87601;

XX 26-OCT-1999 (first entry)

XX Mouse sodium channel NaN cDNA.

XX NaN; sodium channel; ion transport; mouse; dorsal root ganglia;
KW pain; paraesthesia; hyperexcitability; therapy; Scn1a gene; ss.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 19..5316

XX misc_feature 4201..4260

XX /tag= a

XX /tag= b

FT /note= "these bases represent nucleotides missing
FT from the sequence given in Fig 7 of the
FT specification. The nucleotides are
FT included to maintain the nucleotide
FT numbering given in the specification for
FT this DNA sequence"

FT polyA_signal 5789..5794

/*tag= c

WO938889-A2.

05-AUG-1999.

29-JAN-1999; 99WO-US02008.

20-NOV-1998; 98US-0109402.

29-JAN-1998; 98US-0072990.

(UYXA) UNIV YALE.

Dib-Hajj S, Waxman S;

WPI; 1999-479168/40.

P-PSDB; AAY06597.

New isolated nucleic acids encoding sodium channels, used to develop
products for treating acute or chronic pain or hyperexcitability
phenomena

Claim 1; Fig 7A1-3; 9lpp; English.

This is the nucleotide sequence of an isolated nucleic acid which
encodes the mouse NaN channel (see AAY06597), a previously unidentified
voltage gated sodium channel protein that is preferentially
expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and
which produces a TTX-R sodium current. The NaN channel cDNA was
obtained from mouse trigeminal ganglia cDNA by PCR amplification
using rat NaN-based primers (see AAX87618-19). Rat, mouse and human
NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98)
are provided. The invention also includes expression vectors and
transformed host cells, methods for identifying tissues and cells
that express NaN, methods for identifying agents that modulate NaN
channel activity or NaN channel mRNA transcription or translation,
and a method for using such agents to treat acute or chronic pain,
paraesthesia and hyperexcitability phenomena. The preferential
expression of NaN in sensory DRG and trigeminal neurons provides a
target for selectively modifying the behaviour of these nerve cells
while not affecting other nerve cells in the brain and spinal cord.
The gene encoding NaN has been named Scn1a.

Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 61 other;

Query Match

Best Local Similarity 77.6%; Score 4573.8; DB 20; Length 5822;

Matches 5133; Conservative 0; Mismatches 663; Indels 78; Gaps 12;

QY 40 aggggtgaagatggagagaggttactaccggtgtatcttcccgagacagaggaattccgcg 99

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 10 aggggtgaagatggagagaggttactaccggtgtatcttcccgagacagaggaattccgcg 69

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 100 cccttcacttcgactctctgctgccataaagaagcgaattgtctcaaaaggagag 159

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 70 cccttcacttcgactctctgctgccataaagaagcgaattgtctcaaaaggagag 129

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 160 aagaagtcacaaagacagcggcagctgagcccgctgagcccgctgagcttgacctaaag 219

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 130 aagaatccaaagacagcggcagcgaactgagcccgctgagcccgctgagcttgacctaaag 189

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 220 gcttcaggaaagttaactaagctttatgtagacattccccctgagcttgttagaaccct 279

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 190 gcttcaggaaagttaactaagctttatgtagacattccccctgagcttgttagaaccct 249

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 280 ctggaggacctgacccctactactaagaacacataaagacattcatgtgttgaacaagaa 339

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 250 ctggaggacctgacccctactactaagaacacataaagacattcatgttgaacaagaa 309

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QY 340 agaacaattatgcttcagcgcgaagcggcctgttcaattctggggccttttaacc 399

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 310 agaacaattatgcttcagcgcgaagcggcctgttcaattctggggccttttaacc 369

[illegible][illegible]

QY 4771 gtggtcaacatgtacatcgctgtgatctctcgagaacttcaacacagccacggaggagc 4830
DB 4741 gtggttaacatgtacatagctgtgattctagagaaactcaacacagccacggaggagc 4800
QY 4831 gaggaccctctggaggagcagctttgaaattcttatgaggtctgggagaagtgtgac 4890
DB 4801 gaggaccctctggaggagcagctttgaaattcttatgaggtctgggagaagtgtgac 4860
QY 4891 ccgaggcgtcgagttcaccagttcgcgcctctctgacttgcggagcgcctgcgc 4950
DB 4861 ccgaggcgtcgagttcaccagttcgcgcctctctgacttgcggagcgcctgcgc 4920
QY 4951 gaggcgttgcgtggccagccgaataagtttccagtttctagtgatggacttgcgcctg 5010
DB 4921 gaggcgttgcgtggccagccgaataagtttccagtttctagtgatggacttgcgcctg 4980
QY 5011 gtgagggcgcagcctcattgcatgagttctcttcttcttcttcttcttcttcttctt 5070
DB 4981 gtgagggcgcagcctcattgcatgagttctcttcttcttcttcttcttcttcttctt 5040
QY 5071 ggggactccagcgtctgataccatgaaacacatgagagagagagtttatggagcc 5130
DB 5041 ggggactccagcgtctgataccatgaaacacatgagagagagagtttatggagcc 5100
QY 5131 aacccttttaagaagctctacgagcccatagtcaccaccacacagagagagagagag 5190
DB 5101 aacccttttaagaagctctacgagcccatagtcaccaccacacagagagagagagag 5160
QY 5191 caaggcgcgcgtctacacagagggcctaccggaacacacatgagagagagagagag 5250
DB 5161 gaagtgcgcgtctacacagagggcctaccggaacacacatgagagagagagagag 5220
QY 5251 agctgaagagacaggtcaagtctacgcacaggtgttttgcattgagagagagagag 5310
DB 5221 agctgaagagagaggtcaagtctacgcacaggtgttttgcattgagagagagagag 5280
QY 5311 ttgaggtggccaggttcaaggttcaaatgactg-aacctcatctccaccctaccctc 5369
DB 5281 ttgaggtggccaggttcaaggttcaaatgactg-aacctcatctccaccctaccctc 5340
QY 5370 actgctcaacagtttagctctcagcctctgcgagagggcgagagactcactgaacacag 5429
DB 5341 acagctcaacagtttagctctcagcctctgcgagagggcgagagactcactgaacacag 5398
QY 5430 gccgttcgactgtgttttggctgaacgaggtgacaggttgccgtccatttttaaatga 5489
DB 5399 gccgttcgactgtgttttggctgaacgaggtgacaggttgccgtccatttttaaatga 5458
QY 5490 ctcttggaaagatttctatgagagatgttagaaggagctgcaaaagacacagcaccata 5549
DB 5459 ttcttggaaagatttctatgagagatgttagaaggagctgcaaaagacacacagta 5518
QY 5550 acggaagcctctgagagacagctccaaactacataaagatgagaacaaagaaagatcc 5609
DB 5519 acggaagcctctgagagacagctccaaactacataaagatgagaacaaagaaagatcc 5573
QY 5610 caggaaacttcagattgtttctcagatattcccaatgtgtctgttcgggttttga 5669
DB 5574 catg-----tcgttcagattttta 5592
QY 5670 gtagtgacctgcacatgtagctcttttttgcagtac-----gtcaaacacctgcag 5723
DB 5593 gtagtgacctgcacatgtagctcttttgcagtac-----gtcaaacacctgcag 5652
QY 5724 taagttaataagc-ttgctacgggtgttctcaccagatcaccagaaatgggtgtatgactc 5782
DB 5653 taagttaataagc-ttgctacgggtgttctcaccagatcaccagaaatgggtgtatgactc 5712
QY 5783 aaacctaaagatgactctgactgttcagtcagcaccctcagacttttcagagcgtccaatc 5842
DB 5713 aaacctaaagatgactctgactgttcagtcagcaccctcagacttttcagagcgtctgac 5768

QY 5843 tctgtcccgaggtgtcttaacgaataaataagtgtaaaagaaaaa 5896
DB 5769 tctgtcccgaggtgtcttaacgaataaataagtgtaaaagaaaaa 5822
RESULT 8
AAF30101 ID AAF30101 standard; cDNA; 5860 BP.
XX AAF30101;
XX AC AAF30101;
XX DT 30-APR-2001 (first entry)
XX Human sodium channel Na^v cDNA.
XX Sodium channel; Na^v: human; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
KW diagnosis; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
ET CDS 31..5402
ET /*tag= a
XX WO200105831-A1.
XX 25-JAN-2001.
XX 14-JUL-2000; 2000WO-US19342.
XX 16-JUL-1999; 99US-0354147.
XX (UYA) UNIV YALE.
XX D1b-Hajj S, Waxman SG;
XX WPI; 2001-103147/11.
XX P-PSDB; AAB20121.
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -
XX Claim 1; Fig 11A; 162pp; English.
XX The present sequence is that of cDNA encoding a novel human tetrodotoxin resistant sodium channel, termed Na^v (see AAB20121). The cDNA was isolated from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also AAF30122-23). Na^v belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of Na^v on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through Na^v channels, or which modulates transcription or translation of Na^v mRNA, in dorsal root ganglia or trigeminal neurons. Na^v nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate Na^v expression, in the diagnosis of disease, and in the recombinant production of Na^v polypeptides.
XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 other;

Query Match 55.0%; Score 3242.6; DB 22; Length 5860;
Best Local Similarity 76.2%; Pred. No. 0;

Query Match 36.7%; Score 2162.8; DB 22; Length 3701;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 2804; Conservative 0; Mismatches 837; Indels 69; Gaps 7;

Qy 637 ttcattgcatgaaacagcgatgcgaactgttttccggcgagcccaagtcacattcttca 696
Db 1 tccattgcatgaaacagcgatgctcatatattccaggaaatccacatcaactattg 60
Qy 697 gctcttgatccctccagagtggtcagagctcgaagcgatttcagttatcaggtctg 756
Db 61 cccctgctacctcccgtggttcagagcttgaaagcaatttcagtagtttcacgtctg 120
Qy 757 aaggtcatcgttagtgccctgctgcgtcggtgaagagcttggtagacgtgagtgctc 816
Db 121 aaggtcatcgtggggcctgctacgctcgtggaagcgtggtcaacggtattatcctc 180
Qy 817 actctcttgcctcagcatctttgcccctggctgcagagcgtggttcagtggttggaattctg 876
Db 181 acctctttgctcagcatctttgcccctggtaggtcagcagctcttcattgggaagtctg 240
Qy 877 aaccagagtgatataagcacaaactg-----tgcccccaacctgcatacaagat 930
Db 241 aacctgaatgcatcctcgaggagctgtaaaaatactagtaacccggagccttatgacct 300
Qy 931 tgctttgaaaagaaaagatagcgaagacttcataatgtgtgtacgtcgtcggcagc 990
Db 301 tgctttgaaaagaaaattccactgaattcaaaatgtgtggtcattcgtggtgaac 360
Qy 991 agaccctgtcccaatggtttacgtgcgcgataaaacacattgaacccagacataattat 1050
Db 361 agtgcctgttccacacataatgaatgaagcacacaaaattaatcctgcataattat 420
Qy 1051 acaagtttcaaacatttgctgtctcttcctgcctgcctgcttcctgggttatgaactcaagac 1110
Db 421 acgaatttgaacacttggctgtctcttctgcccgtgttcctgcctggtgcgcagacccaagat 480
Qy 1111 tccctggagaggtcttaccgacagatcctcggaacctctggtgactcttctgtcttctc 1170
Db 481 tccctggagaggtttatcaacagaccctgcgtactactggtcctactcagttctcttc 540
Qy 1171 ttctggtgttcacttctcctgggtctcttctacgttgcattacctaaccctggctgtctc 1230
Db 541 ttctggtgttcacttctcctgggtctcttctacgttgcattacctaaccctggctgtctc 600
Qy 1231 acctggttatgagacagaaacagaaatgtagtctgcagacagagggccaagagaaa 1290
Db 601 acctggttatgagagagcagaaacagaaatgtagtctgcagagatagagggccaagagaaa 660
Qy 1291 atgtttcagaagcccagcagctgttaaggagagagagaggtcctggttgccatggga 1350
Db 661 atgtttcagaagcccagcagctgttaaggagagagagaggtcctggttgccatggga 720
Qy 1351 attgacagaagttcccttaattcccttcagcgttcactcttctcccgagaaagagaaag 1410
Db 721 attgacagaagttccacttacttctcctgaaacatcatattttacccccaaaaagagaaa 780
Qy 1411 ttttcggttagtagacaaagaaagtcctcttcttatgaggggtccagagggcccaagcc 1470
Db 781 cctcttggttaataagaaaagaaagccctcttcttggagaggtcgtggaaagaccagcct 840
Qy 1471 tcagcgtctgattcagaggacgaagcctctaaaaatccacagctccttgagcagacaaa 1530
Db 841 cctgggtcagattctgatgaagtgcacaaaagccacagctccttagagcaaacccaaa 900
Qy 1531 cgaactgccagaactgcccagtggaatctctttgatgagcagctggagcccccctccacag 1590
Db 901 cgaactgccagaatctatcaytggaacactttgatgagcagtgagatcctctcccaag 960
Qy 1591 cagagagcgtcagcgtgctgagttatcttaaccatcaccatacaggaacaaagaaaattc 1650
Db 961 cagagagcgtgagtgctcagcatcctcaccatcaccatgaagggaacaaagaaaatca 1020

Qy 1651 caggagcctgtttcccatgtgggaaaaaatttggcctctaagtagtaccctgggtgggaactgt 1710
Db 1021 caagagcctgtctccctgttgggaaaaacctggcaccagtagtaccctgtgtggaactgt 1080
Qy 1711 agcctcagtggtgtgcatataaagaaggtcctgcggaccatcatcagcagatccctttact 1770
Db 1081 tgccccagtggtgtgcttaagaaggtcctgagaactgtgtagctgagccgtttact 1140
Qy 1771 gagctggccatccacatcctcatcatcaataaccgtttctcttagcgtgagacacac 1830
Db 1141 gagctggccatccacatcctcatcatcaataaccgtttctcttggccatgagcacaac 1200
Qy 1831 aacatgtagacaaacttaagaccatctgaaaaatagaaaaactgggtttttcacgggaatt 1890
Db 1201 aagatggaggcagttttgagaagatgttgaatatagggaatttgggttttctactagcatt 1260
Qy 1891 ttcatagcggaaatgtgtctcaagatcatcgctgcgtcgaaccttaccactacttccggcac 1950
Db 1261 ttatagcagaatgtgcttaaaaatcattgcgtcgcgcacccctaccactacttccgcga 1320
Qy 1951 ggctgggaatgtttttgacagcatcgtggccctcctgagtcgctgagtcgtgctctacaac 2010
Db 1321 ggctgggaacatttttgacagcattgtgtctctctgagtttgcagatgttaataactgt 1380
Qy 2011 acactgtctgataacaataggtcttttggcttccctcagagtgctgagggctctcaag 2070
Db 1381 gtacttcaaaagagaagctggccactcttggttccctcagagtgctcagggctctcaag 1440
Qy 2071 ttacgcaaatcctggcccaactttaaacaactctcattaaagatcactcggccactcctgggc 2130
Db 1441 ttacgcaaatcctggcccaacttgaacacactaataagaataatcggcaactctgcgga 1500
Qy 2131 gcgcttgaaaacctgactgtgtcctgactatcgtgtgtcttctcattcttctgtgtgagc 2190
Db 1501 gcccttggaaagcctgcagctggtgtcctggtcattgtgattcttctctcagtgagtggc 1560
Qy 2191 atgcggtcttcggcaccaactttaa--caagacgcctcagcaccacagagcggccca 2248
Db 1561 atgcagcttttggccgtagcttcaattcccaaaagagtccaaaactctgtaacccgaca 1620
Qy 2249 gg-----cgcgctggcacatgataaattctctaccactctctctc 2289
Db 1621 ggcccgacagtctcatgtttacggcactggcacatggggatcttctggcactctctcta 1680
Qy 2290 gtggtgttcgcactcctctgtgggaaatggatcgagaacatgtggggctgcgcagat 2349
Db 1681 gtggtattccgcactcctctgcgggaaatggatcgaaaatactgtgggaatgcatcaagaa 1740
Qy 2350 atggagc---gctcccgttgtgcatactattgtctcttgcctgataaattggtgatcggaag 2406
Db 1741 gcgaatgcatacatcatattgtgttattgtctctcatattgatacaggtgataggaata 1800
Qy 2407 ctttgtgtgttaacctcttctcattgctgtgtcgtcgaattcctcagcaatagagagaag 2466
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Qy 2467 gatgggacgttggaagagagaccagaaaaaaccaaatgcagctagcctgagctggttc 2526
Db 1861 aatggaaacttagaagagagagccagaaaaactaaagccagttagcactggaatcgatctc 1920
Qy 2527 cgccgggctctctctcattcgtcagcgtcttcagagtttttctgcaagaaatgcagg 2586
Db 1921 cgccgggcttttctgttgtagacacactcttgagcattctctgcaaatggtgcagg 1980
Qy 2587 aggaaaaactgcgcaagccaaaagagacaaacagaaagcttctgtgtgagaaataaagac 2646
Db 1981 aagcaaaacttaccacagcaaaaagagtggcagagaggtgctgctgcacaaagcaaacac 2040
Qy 2647 tcaatctcccgatgcagagccctggaagagatgatac----- 2687
Db 2041 atcattccccctgttcatggtgagatgaaaagggggtccagagaccagagaggtctgtata 2100
Qy 2688 -----agacatggctttgtacactggacagggcggtggtcgtcggtggtcccaactc 2736

CC for a portion (see AAY06596) of human Nan, a previously unidentified
 CC voltage gated sodium channel protein that is preferentially
 CC expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and
 CC which produces a TTX-R sodium current. The Nan channel cDNA was
 CC obtained from human DRG tissue cDNA by PCR amplification (see also
 CC AAX87620-22). Rat, mouse and human Nan nucleic acids (see AAX87600-02)
 CC and polypeptides (see AAY06596-98) are provided. The invention also
 CC includes expression vectors and transformed host cells, methods for
 CC identifying tissues and cells that express Nan, methods for
 CC identifying agents that modulate Nan channel activity or Nan
 CC channel mRNA transcription or translation, and a method for using
 CC such agents to treat acute or chronic pain, anaesthesia and
 CC hyperexcitability phenomena. The preferential expression of Nan in
 CC sensory DRG and trigeminal neurons provides a target for
 CC selectively modifying the behaviour of these nerve cells while not
 CC affecting other nerve cells in the brain and spinal cord. The
 CC gene is named SCN11a.
 XX
 SQ Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 1 other;

Query Match 34.8%; Score 2050.8; DB 20; Length 3638;
 Best Local Similarity 74.3%; Pred. No. 0; Mismatches 822; Indels 132; Gaps 8;
 Matches 2756; Conservative 0;

QY 637 ttcattgtcattggaacagcagatcgcaactgttttccggcgagccaagtcaatcttca 696
 DB 1 tccattgtcattggaatagcagattgtgtcatatattccaggaatcaccatcaacttg 60
 QY 697 gctcttgtaacctccagtggttcagagctctgaagcgatttcagttatctcaggtctg 756
 DB 61 cccctgcgtacctccggtgttcagagctttgaagcaatttcagtagtttcacgtctg 120
 QY 757 aaggtcatcgtagggtccctgcgtcgtgtaaaagcgtgaacgctgaacgctggtctc 816
 DB 121 aaggtcatcgtggggcctgtgcacgctgtgtaaaagcgtgtaacgctggtatctc 180
 QY 817 acctcttctgctcagcatcttgcctggtgcgtcagcagctgttcatgggaattctg 876
 DB 181 acctcttctgctcagcatcttgcctggtgagtcagcagcttcttcagggaagctg 240
 QY 877 aaccagaagtgtattagaacaaactg-----tggcccaaacctgcacccaagagat 930
 DB 241 aacctgaattgcattctcgtggggttaaaatatcagtaaacccggaagcttatgaacct 300
 QY 931 tgccttgaagaagaaagatagcgaagacttcaatgtgtgtggtacgtgctcggcagc 990
 DB 301 tgccttgaagaagaaagaaattcacctgaattcacaatgtgtggtcctctggtggtgac 360
 QY 991 agacctgtcccaatggtttacgtgcgataaaacacacattgaaccagacaataattat 1050
 DB 361 agtgcctgttccatacaataatgaatgaagcacacacaaataattactgactataattat 420
 QY 1051 acaaaagttgaacacttggctggtctcttctgcgaatgtccgggttatgactcaagac 1110
 DB 421 acgaattttgaacacttggctggtctcttctgcaatgttccgggtgatgacccaagat 480
 QY 1111 tccgtggagaggtttaccagacagatctcgcgaacctctggaatctacttctcttc 1170
 DB 481 tccgtggagaggtttaccagacagacctcgtactactggtggtctactcagctctcttc 540
 QY 1171 tccgtggtgtctatcttctggctcctcttctacgtcttgaacctgaacctggctgtgtc 1230
 DB 541 ttcattgtggtcatttctctggctcctcttctacgtgatttaacctgaacctggtgtgtt 600
 QY 1231 accatggcttatgaagaacagacaagaatagtagctgctgagacagagcccaaggagaaa 1290
 DB 601 accatggcatatgaggagcagaacaagaatgtagctgacagatagagagcccaaggaaaa 660
 QY 1291 atgtttcaggaaagccagcagctgttaaggaggaggaagagagctgtgttgcctggga 1350
 DB 661 atgtttcaggaaagccagcagctgttaaggaggaggaagagagctgtgttgcctggga 720

QY 1351 attgacagagaagttcccttaattcccttcaagcttcccttcccccgaagaagaag 1410
 DB 721 attgacagagaagttcccttacttcccttgaacatcatatttaccacaaaagaagaag 780
 QY 1411 tttttcgtgtagtaagacaagaagttcttctttatgagaggttcccaagcgcgaagcc 1470
 DB 781 ctctttgttaataagaagaagagtccttctttttagagagagctgtgggaagaccagcct 840
 QY 1471 tcagcgtctgattcagagagcagatgctctataaaatccacagctcttctgacgaccaa 1530
 DB 841 cctgggtccagattctgatgaagattgccaaaaaacacagctctctgagggcaaacaa 900
 QY 1531 cgactgtcccaagaacttgcagctggatctctttgatgagcacgtggagccctccacag 1590
 DB 901 cgactgtcccaagaacttctcaytggaccactttgatgagcatggagatctctccaaag 960
 QY 1591 cagagagcgtgagcgtctcagtatcttataaccataccatacaggaacaagaaaaatc 1650
 DB 961 cagagagcactgagtgctgcagcatctccaccatcaccatgaaggacaagaaaaatca 1020
 QY 1651 cagagcctgtttcccatgtggaaaaatttggccttcaagtacctgtgtggagctgt 1710
 DB 1021 caagagcctgttccctctggtgagaaaacctggcaaccaagctccctgtggagactgt 1080
 QY 1711 agcctcagtggtgtgcataaaagaaggtcctcgggaccatcatgacggatccctttact 1770
 DB 1081 tgcctccagtggtgtgcttaagaaggtcctcagaaactgtgactgactgacccgtttact 1140
 QY 1771 gactggcctaccatctgcatactcaataaccgttttcttagcgttggagacacac 1830
 DB 1141 gactggcctaccatctgcatactcaataccactgtcttctggcctggagatcac 1200
 QY 1831 aacatggatgacaacttaagaacatactgaaaaataggaactgggttttcacgggaatt 1890
 DB 1201 aagatggagccaggttttgagaagatgttgaaataaggggaatttggtttctcactagat 1260
 QY 1891 ttcataggcgaataatgtgttcaagaatcgcgtgcgcaccttaccactacttccggcac 1950
 DB 1261 tttatagcagaataatgtgcctaaaaatcattgcgtcgtacctaccactacttccgcga 1320
 QY 1951 ggcgtgaatgttttgacagcagatcgtggcctcctcgtgactgctgactgctctacaac 2010
 DB 1321 ggcgtgaacattttgacagcattgtgtctctctgagtttgcagatgtaatagaactgt 1380
 QY 2011 acactgtctgatacaataatggttcttctggttccctcagagctgctgaggttctcaag 2070
 DB 1381 gtacttcaaaagagaagctggccattcttgcgttctcctcagagctgctcaggggttctcaag 1440
 QY 2071 tttagcgaatctctggccacgtttaaacactctcattaaagatcatcggccactcctgggc 2130
 DB 1441 tttagcgaatctctggccacgtttaaacactctcattaaagatcatcggcaactctgcga 1500
 QY 2131 gccttggaaaactgactgtggtcctcgtactatcgtggttctcacttcttctgtgtgtggc 2190
 DB 1501 gccttggaaagcgtgactgtggtcctggtgctattgtgactcttatttctcagtagttggc 1560
 QY 2191 atgcggtctctcggcacaagtttaa--caagaccgctcagccacacagagcgccca 2248
 DB 1561 atgcagcttttggcgtagcttcaattcccaaaagagtcacaaactctgtaacccgcga 1620
 QY 2249 gg-----cggcgtggcagatgataatttctaccactcctctctg 2289
 DB 1621 ggcgcagactctcatgtttacggcactggcactggggaattcttctgcaactcctcta 1680
 QY 2290 gtggtgttccgcatctctgtgggaatgagatgagacaatgttgggtgtcagtcagagat 2349
 DB 1681 gtggtattccgcatctctcgtgggaatgagatgagaaaatgttgggaatgtatgcaagaa 1740
 QY 2350 atgagagc---gctcccggttgcatactgcttcttctcctgataatgttgatcggaag 2406
 DB 1741 gcgaatgcatcatcatctgtgttattgtctctcattgttgcagcgtgatagggaaa 1800
 QY 2407 ctgtgtgtgttaacctcttcaattgctgtgctcattctctcagcaaatgagagagaag 2466

[illegible]

DB	2815	tccagtttgaaagaaatgaaggtgggtgcattgctctcatagtgccataccctgccatt	2874
QY	3517	ctcaatgtctgtgctgctgcctcattctctgctgcgtattttgtctatctctgaggagtaaat	3576
DB	2875	ctgaatgtctgtgctgctgcctcattctctgctgcgtattttgtctatctctgaggagtagac	2934
QY	3577	ttatttctgggaagtttggaagtgcatctaacgggacagacataaataatgtatttggat	3636
DB	2935	ttcttctggaaaatttgggaaaatgcattaatgaacagactcagtta-----taaat	2988
QY	3637	ttaccgaagtctccgaaccgagccaatgtaacattagtaattactctcgaggaggtcccg	3696
DB	2989	tataccatcattacaataaaaagtcaatgtgaagtggcaatttctcttggatcaaccag	3048
QY	3697	caggctcaacttgacaacgtggggaalgcctatctgcctctgctgcgaatggtgcaacctat	3756
DB	3049	aaagtcaacttggacaatgtgggaaaatgcttacctgcgtctgcctgcaagtggcaacctt	3108
QY	3757	aagggtcgtcggaaatcatgaatgctgctgtcgattccagagagagaagaacagacgcg	3816
DB	3109	aagggtcgatggatattatataatgcagctgttgattccacagagaagaacaacagcca	3168
QY	3817	gaacttgaggcgaacctctacgcgtatctctactttgtgttttatcatctctcgctcc	3876
DB	3169	gagtttgagagcaattcaactcggttacatttactctgtagtctttatcatcttggctcca	3228
QY	3877	ttcttacctgaacctctttatcgtgttatattgacaacttcaatcagcagcagaaa	3936
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QY	3937	aagttagggtgccaaagacattttatgcagaagaacagaagaataattacaatgcgaatg	3996
DB	3289	aagttagggtgccaaagacattttatgcagaagaacagaagaataactataatgcgaatg	3348
QY	3997	aaaaagttagaaccagaacactcaaaagcccatcccaaagcccctgaaacaaatgtcaa	4056
DB	3349	aaaaaattaggattccaaaaaacctcaaaacccattccacggtctcgaaacaaatgtcaa	3408
QY	4057	gccttgtgttcgaacctgtcaaacgcaggtctttagtcgtcatcttctgggtcttatt	4116
DB	3409	ggctctgtgtcagacatgtcacaagccagaaccttgagatcaatcaatgaatgctcatt	3468
QY	4117	gtcttaaatatgatattcatgatggctgaatctgcgaccagcccaagaatgtgaagaaa	4176
DB	3469	atcctaaacatgattagatgatgctgaatcatacaaccaacccaacgaatgataatcc	3528
QY	4177	acctttgatatctctcaacatagccttctgtgttcattttaccatagagtgctcatcaaa	4236
DB	3529	atccttgaaacctcaactgggtcttctgtgttcattctttagcttagaattgctcatcaaa	3588
QY	4237	gtcttctgtttgaggcaacactacttccaccaatgctcgaacttatttga	4296
DB	3589	atcttctgtttgaggcaatcactacttccaccaatgctcgaacttatttga	4348

RESULT 11

AAAF57009
ID AAAF57009 standard; cDNA; 6344 BP.

AC AAF57009:

14-MAY-2001 (first entry)

Rat PN3 cDNA sequence.

peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit.

peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;
peripheral nerve tetrodotoxin-resistant sodium channel type 3; PN3; rat;
tetrodotoxin; TRX; peripheral nerve sodium channel type 3; PN3; rat;
sodium channel protein; peripheral nervous system; allodynia; neuropathy;
hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulneryary;
analgesic; anti-HIV; ss.

Rattus sp.

3 XX

Key Location/Qualifiers
CDS 23..5893
/*tag= a
/product= "PN3"

US6184349-BL.
06-FEB-2001.
15-APR-1997; 97US-0843417.
11-OCT-1995; 95US-0511828.
(SYNT) SYNTEX USA INC.
Herman R, Delgado SG, Fish LM, Sangameswaran L, Rabert DK;
WPI: 2001-202004/20.
P-PSDB; AAB61995.
New rat and human tetrodotoxin-resistant, voltage-gated sodium channel proteins, present in peripheral nerve tissue, useful as a therapeutic target for compounds treating peripheral nervous system disorders -
Example 2; Fig 1A-I; 86pp; English.
The invention provides purified and isolated rat and human peripheral nerve tetrodotoxin (TTX)-resistant sodium channel type 3 (PN3) protein or its human homologues are useful for the development of antibodies against PN3 which are useful in affinity chromatography to purify recombinant sodium channel proteins or polypeptides, or as a research tool. The PN3 proteins are useful as therapeutic targets for compounds to treat disorders of the peripheral nervous system such as allodynia, hyperalgesia, diabetic neuropathy, traumatic injury and acquired immunodeficiency syndrome (AIDS)-associated neuropathy. The present sequence represents the cDNA encoding the rat PN3 protein.
Sequence 6344 BP; 1487 A; 1823 C; 1622 G; 1412 T; 0 other;

Query Match 23.9%; Score 1411.4; DB 22; Length 6344;
Best Local Similarity 57.6%; Pred. No. 0;
Matches 3248; Conservative 0; Mismatches 1921; Indels 474; Gaps 21;
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KW neuropathic pain; glia; muscle; parasympathetic nervous system;
KW enteric nervous system; central nervous system; dorsal root ganglia;
XX cranial ganglia; ss.

OS Rattus rattus.

XX Key Location/Qualifiers
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FT /label= C>G
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FT /note= "Causes Val > Ile substitution"
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FT 1964
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FT /note= "Causes His > Asp substitution"
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FT /note= "Addition of AAA"

XX WO9701577-A1.
XX 16-JAN-1997.
XX 25-JUN-1996; 96WO-GB01523.
XX 28-JUN-1995; 95GB-0013180.
XX (UNLO) UNIV COLLEGE LONDON.
XX Akopian AN, Wood JN;
XX WPI; 1997-100165/09.
DR P-PSDB; AAW21740.

XX
PT
PT
PT
XX
PS
XX

New isolated mammalian sensory neuron sodium channel protein - used to identify modulators of the sodium channel, partic. for the treatment of pain

Claim 9; Page 85-93; 128pp; English.

The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This sequence contains 12 nucleotide differences to the wildtype rat DRG(SNS-B) (see also AAT77803) causing nine amino acid changes.

Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T; 0 other;

Query Match 23.8%; Score 1405.2; DB 18; Length 6527;
Best Local Similarity 57.5%; Pred. No. 0;
Matches 3246; Conservative 0; Mismatches 1923; Indels 477; Gaps 21;

QY 45 gaagatggagggaggtactaccggtgatcttcccgagcagcgaggaattccgccctt 104
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RESULT 14
AAF57016
ID AAF57016 standard; CDNA; 5874 BP.
XX
AC AAF57016;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human hPN3 cDNA sequence.
XX
KW Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;
KW tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; human;
KW sodium channel protein; peripheral nervous system; allodynia; neuropathy;
KW hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnery;
KW analgesic; anti-HIV; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 1..5871
FT Location/Qualifiers
FT /*tag= a
FT /product= "hPN3"
XX
PN US6184349-B1.
XX

PD 06-FEB-2001.
XX
PF 15-APR-1997; 97US-0843417.
XX
PR 11-OCT-1995; 95US-0511828.
XX
PA (SYNT) SYNTEX USA INC.
XX
PI Herman R, Delgado SG, Fish LM, Sangameswaran L, Robert DK;
DR WPI; 2001-202004/20.
XX P-PSDB; AAB61996.
PT New rat and human tetrodotoxin-resistant, voltage-gated sodium channel
PT proteins, present in peripheral nerve tissue, useful as a therapeutic
PT target for compounds treating peripheral nervous system disorders -
XX Disclosure; Fig 5A-K; 86pp; English.
XX
CC The invention provides purified and isolated rat and human peripheral
CC nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins.
CC The rat peripheral nerve sodium channel type 3 (PN3) protein or its human
CC homologue are useful for the development of antibodies against PN3 which
CC are useful in affinity chromatography to purify recombinant sodium
CC channel proteins or polypeptides, or as a research tool. The PN3 proteins
CC are useful as therapeutic targets for compounds to treat disorders of the
CC peripheral nervous system such as allodynia, hyperalgesia, diabetic
CC neuropathy, traumatic injury and acquired immunodeficiency syndrome
CC (AIDS)-associated neuropathy. The present sequence represents the cDNA
CC encoding the human hPN3 protein.
XX
SQ Sequence 5874 BP; 1434 A; 1553 C; 1428 G; 1459 T; 0 other;

Query Match 23.5%; Score 1384.4; DB 22; Length 5874;
Best Local Similarity 57.3%; Pred. No. 0;
Matches 3227; Conservative 0; Mismatches 1956; Indels 477; Gaps 21;
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19	633	10.7	6318	2	US-08-808-793-1	Sequence 1, Appli
20	633	10.7	6318	3	US-08-772-512A-1	Sequence 1, Appli
21	630.2	10.7	6315	2	US-08-808-793-2	Sequence 2, Appli
22	630.2	10.7	6315	2	US-08-772-512A-2	Sequence 2, Appli
23	374.4	6.3	930	3	US-08-605-284B-21	Sequence 21, Appli
24	373.2	6.3	930	3	US-08-605-284B-1	Sequence 1, Appli
25	373.2	6.3	930	3	US-08-605-284B-3	Sequence 3, Appli
26	368.4	6.2	902	3	US-08-605-284B-2	Sequence 2, Appli
27	292.2	5.0	702	4	US-08-843-417-3	Sequence 3, Appli

Query Match 23.9%; Score 1411.4; DB 4; Length 6344;
Best Local Similarity 57.6%; Pred. No. 0; Mismatches 1921; Indels 474; Gaps 21;
Matches 3248; Conservative 0;

QY	45	gaagatgagagagaggtactaccgggtgattctccggagcagcgggaattccgcgcctt	104
DB	10	GAAGAATGAGAAGATGAGCTCCCTTTGCGTCCTGGGAACATACCAATTTACAGCGTT	69
QY	105	caattcagactctctggtgctcctaagaagcggattgctatccaa-----aa	152
DB	70	CACCTCCAGAGTCACTGGCAGAGATCGAGAAGCAGATTTGCTGCTCACCGCGCAGCCAA	129
QY	153	ggagagaaagaactcacaagacagcggcagctgagcccccagcctcgccctcagcttga	212
DB	130	GGCCAGAACCAACAGACAGAGGAGGAGCAAGGGGAGGAGCCCGAGGCTCAGCTGGA	189
QY	213	ccctaaagcctcaggaagttaacctaaagctttatggtgacattccccctcagctgttac	272
DB	190	CTTGAAGCCTGTAAACAGCTGCCAAGTTCATGTGTGAGTCCACAGCAGAACTGGTCG	249
QY	273	gaacctctgagagacctgagccctactacaaagaccataagaacattcatgtgtgaa	332
DB	250	GGAGCCCTGGAGACCTAGACCCCTTTCTACAGCACACACCGGACATTCATGTTGAA	309
QY	333	caagaaagaacaattatcgcttcagccgcaagcggccttattcattctgggcttt	392
DB	310	TAAAGCAGGACCATTTCCAGATTCAGTGCCACTTGGGCCCTTGCGCTCTTCAGTCCTT	369
QY	393	taatccccctcagaagcttaattgattctctctgctccattcagcttcttagcattcat	452
DB	370	CAACCTGATCAGAAGAACACGCCATCAAGGTCTGTCTCATTCCTGGTCTCCATATTCAT	429
QY	453	catctgcacggtgatactcaactgtatggttcattgaggaattctatggagagaagttcga	512
DB	430	CACCATCATATTTTGGTCAACTGCGTGTGCATGACCC-----GAACGTGATCT	477
QY	513	caacgacattccccgaatcacgtcttcatggatttatattttagaagctgtgattaaat	572
DB	478	TCAGAGAAAGTCGAGTACGTCTTCACTGTCTCATTTACACCTTCGAGGCTCTGATTAAGAT	537
QY	573	attggcaagaggttcaattgtgagtttctctctccctccgagatcgtgggaactggct	632
DB	538	ACTGGCAAGAGGTTTGTCTAAATGAGTTCACCTTATCTTCGAGATCCGTGGAACGGCT	597
QY	633	ggacttcattgtcattggagacagcagtcgcaactgtttcccgggagcgaagtcaatct	692
DB	598	GGACTTCAGTGTCTATACCTTGGCGTATGTGGGTGCGAGCATAGACCTCCGAGGAA---T	654
QY	693	ttcagctctctgacactccaggtgttcagagctctcgaagcggatttcagttatctcagg	752
DB	655	CTCAGGCTCGGACATTCGAGTTCACAGGCCCTGAAACATGTTTCTGTGATCCGAGG	714
QY	753	tcgaaggtcatcgtaggtgctctgctgctcgtggtgaaagaagctgtgagacgtgaggt	812
DB	715	ACTGAAGTCACTCGTGGAGCCCTGATCCACTCAGTGAAGGAGTGGCCGACGTGACTAT	774
QY	813	ccctcactctctctgctcagcattcttgcctgggttcagcagctgttcattggaat	872
DB	775	CCTCACAGTCTCTGCTGAGCGTCTTCGCGCTTGGTGGGCTGCAGCGTCTTAAAGGGAA	834
QY	873	tcgaaccaaagaagtattaaagacaaactgtggcccaacccctgcacccaac-----	924
DB	835	CTTTAGAACAAATGATCAGGAACGGAACAGATCCCCCAAGCTGCACACCTCTCATC	894
QY	925	-----aagattgctttgaaaggaagaaagatagcgaagacttcaaatgtgtgtac	977
DB	895	TGAAATGGCAGATACATCTTCATCAAGCCTGGTACTACGGATCCCTTACTGTGCGCAA	954
QY	978	ctggctcggcagcagaccctgtcccaatggttcttaoatgctgaataaaacacattgaaccc	1037
DB	955	TGGGTCTGATGCTGGTCACTGCCCTGGAGGCTATGTCTGCTGAAAACTCCTGACAAACC	1014
QY	1038	agacaataattatacaaaagtttgaacactttggctggtcctttctcgcacatgttccgggt	1097
DB	1015	GGATTTAACTACACAGCTTTGATTCCTTTGGCTGGGCATTCCTCTACACTGTTCGCGCT	1074
QY	1098	tatgaactcaagactcctcggagaggtttaccgacagatcctcggagacctctggatcta	1157
DB	1075	CATGACGACGAGCTCCTGGGAGCGCTGTACCAGCACACACTCCGGGCTTCTGGGAAAT	1134
QY	1158	ctttgtcttcttctggtggtcctctcctcctggtggtccttcttctacactgttaacctaac	1217
DB	1135	GTACATGGCTTTTTCGTGCTGTATTTTCTTGGATCGTTTACCTGTGTCATTTGAT	1194
QY	1218	cctggctgtgtcaccatgcttatgaagacagacagaaaatgtagctcgtgagacaga	1277
DB	1195	CTTGGCCGTGTCACCATGGGTATGAAGACAGAGCCAGGCAACAATTCGAGAAATCGA	1254
QY	1278	ggccaagagaaaaatttttcagaaagcccagcagctgttaaggagagagaaggaggtct	1337
DB	1255	AGCAAGGAAAAAAGTTCCAGGAAGCCTTTGAGGTGCTGCAGAAGGAACAGGAGGTGCT	1314
QY	1338	ggttgcatgggaattgacagaagttcccttaattcccttcaagcttccatcttccccc	1397
DB	1315	GGAGCCCTGGGATTTGACACGACCTCGCTCCAGTCCACAGTGGATCACCTTAGGCTC	1374
QY	1398	gaagaa-----gaggaagtgttctggtagtaagaacaaagaagtctcttcttatgaga	1449
DB	1375	CANAAGCCCAANTGAGAGAAGACCCAGGGTGAATCAAGGGTGTACAGAGGCTCCACGGA	1434
QY	1450	gggtccaaagcggcccaagcctcagcgtctgattcagagacgagctcctctaaatacca	1509
DB	1435	TGACAACAGGTCAACCCCAATTCGACCTTACAACACGCGCAGGATGTCTTTCCCTAGGCT	1494
QY	1510	cagctccttga-----gcagaccaaagcagctgtcccagaacttgcca	1551
DB	1495	GTCTTTCAGGAAGACGACGAGGCTAGCCACGCGAGTGTCTTCCACTCCGAGCGCCGCCA	1554
QY	1552	gtgagctctt-----	1562
DB	1555	AGCATCTCATTTCTCAGCGGATCACGGATGATGGGGTCTTTTCACGAGNCCAGGAAG	1614
QY	1563	-----tgatgacacgtggacccctccacagg--	1590
DB	1615	CCGTGAGGTTCCATATTGCTGGCAGGGTGTCTGGCAGACAGGTCCACTCCCCAGGAG	1674
QY	1591	-----	1590
DB	1675	CCCACTGCCCTCAGTCCCCCAACCTTGCCCGTAGACATGGAGAACAGGACAGCTCGGAGT	1734
QY	1591	-----	1590
DB	1735	GCCCACTGGTGAGCTTACCCTGGAGCGCTGAAGGCCCGGCACCTCCACACTACAGGGCA	1794
QY	1591	-----cagagagcgtgag	1604
DB	1795	GAAGAGCTTCTGCTGCGGGCTACTTTGAACGAACCTTTCCGAGCACAGAGGGCCATGAG	1854
QY	1605	cgtgtcagtatcttcaaccatcacatcacaggaacaaagaaaaatccacagagcctgttt	1664
DB	1855	CGTGTGATCATGATGATCTTCTGTCTATTGAGAGCTTTGAAGAGTCTAAGCTGAAGTGCC	1914
QY	1665	cccatgtggaaaaatttggcctcctaaagctacgtgtggtgagactgtagcctcagtgct	1724
DB	1915	ACCTGCTTGTATCAGCTTCGCTCAGAAGTATCTGATCTGGAGGTCTGCCCAAGTGGAG	1974
QY	1725	gtgcataaaagaagctcctcgggaccatcatgacgagatccctttactgagctgagctcac	1784
DB	1975	GAACTTCAAGATGCGCTGTTCGAGCTGGTGAAGTGAACCTTTCCGAGAGCTTACCATCAC	2034
QY	1785	catctgcacatcatcaatccctgtttcttagcgtggagcaccacaaatgagatgacaa	1844
DB	2035	CCTCTGATCGTGGTGAACACCGTCTTCATGGCCATGGAGACTACCCCATGACCGATGC	2094

Db 4246 CTTACCGCTGAATCTCTTTGGGTGCATATCGAGAACTTCAACCAACAGAAAAA 4305
QY 3939 gttagtgcccaagacattttatgacagaagaagaataatatacaatgaa 3998
Db 4306 GTTAGAGGCCAGGACATCTTCATGACAGAAGAGAAAGTACTACAATGCCATGA 4365
QY 3999 aaagttaggaaccaagaacccctaaagcccatcccaagggccctgaacaaatgtcaagc 4058
Db 4366 GAAGCTGGGCTCCAAGAAACCCAGAGCCCATCCACGCCCTGAATAAGTACCAAG 4425
QY 4059 ctttggttgcacctggtcacagccaggtcttttgacgtcatcattctgggtctattgt 4118
Db 4426 CTTGCTGTTTACATCGTACAGGCAAGCCCTTGACATCATCATCTGTTCTCATCTG 4485
QY 4119 ctttaatatgattatgatggtgaatctccgacagcccaagagatgtgaagaaac 4178
Db 4486 CTTCAACATGATCACCATGATGTGGAGACCGACGAGCGGAGGAGAAACAGCAAGT 4545
QY 4179 ctttgatattccatacatagcttggctgctcatctttaccatagagtctcatcaagt 4238
Db 4546 TCTGGGCAGAACTCAACAGTCTTTCTGGCGTCTTTCACGGGCGAGTGTGATGAAGAT 4605
QY 4239 ctttggttgaggcaacatacttaacaaatggtggaactatttgattggtggtg 4298
Db 4606 GTTCGCCCTCGCAGACTACTTCTACCAACGCTGGAACGTGTTCGACTTCATAGTGT 4665
QY 4299 ggtttcttatactagtagtaccctggtt---ccgcttggagacagtgacattcttt 4355
Db 4666 GATCTCTCATTTGGAGTGTGCTGTTTCTTGAATCTTAAAGTCACTCGAAACACTACTT 4725
QY 4356 ccgcccacgctcttcagagtgctgctggtgctcgagtggtcgaaactcctcaggtggt 4415
Db 4726 CTCCCGAGCGCTCTCCGGGTCTATCGTCTGCCAGAGATCGCCGATCTCAGGCTGAT 4785
QY 4416 ccgggtgccccggggaatcagagacctctcttggtttgatgagtctctccctctct 4475
Db 4786 CCGAGCAGCAAGGGATTCGACGCTGCTCTTGGCCCTCATGATGTCCTCGCCGCCCT 4845
QY 4476 cttcaacatgctgctgctctctctctggtggtggttcattacgcacattttgggatgag 4535
Db 4846 CTTCAACATCGGGCTCCTCTCTCTCTGTCATGTTTCACTACTCCTCATCTTCGGCATGCG 4905
QY 4536 ctggtttccaaagtgaagaagggctccgggacgcagcatcttcaacttcgagacctt 4595
Db 4906 CAGCTTCGTAAGCTCGTGACAGAGCCCGCATCGACGATGTTCAACTTCAAGACCTT 4965
QY 4596 taaggcagcatgctgctctcttcagataaacacttcggtggtggatccactct 4655
Db 4966 TGGCAACAGCATGCTGTGCTGTTCAGATCACACCTCGGCCGCTGGGAGCGGCTCCT 5025
QY 4656 caaccccatgct-----ggagggaagaagaacactgcaactcctc 4694
Db 5026 CAGCCCATCTCTCAACACGGGGCTCTCTTACTGCGACCCCAACCTGCCCAACAGCAACGG 5085
QY 4695 ctcccaagacagctgtcagcagccagatagccgctcgtctacttcgttcagttacatcat 4754
Db 5086 CTCGCCGGGGAAGTGGGGAGCCGCGGTGGCATCATCTTCTTCCACCCTTACATCAT 5145
QY 4755 catctctctctcctggtggaacatgtacatcgctgctgacatcgatcgagaacttcaaac 4814
Db 5146 CATCTCTCTCTCATGCTGGTCAACATGTACATCGCAGTGATCTGGAGAACTTCAACGT 5205
QY 4815 agccacggagagagagagacacctctgggagagagacatttgaaattctctatgaggt 4874
Db 5206 GGGCCAGGAGAGAGACGAGCCCTCGAGCGAGGACGACTTCGACATGTTCTATGAGAC 5265
QY 4875 ctgggagaagtgtgacccgagcgctcgcagttcctccagttattcgccctctctgactt 4934
Db 5266 CTGGGAGAAAGTTCGACCCCGAGGCCACCCAGTTTCATGTGCTTTTCTGCGCTCTCAGACTT 5325
QY 4935 tgcgagccctgcccggagccgttgcgttggcccaagccgaataagtttcagtttctagt 4994
Db 5326 CGCGGACAGCTCTCGGGCCCTCTTAGAATCCCAAAACCCAGAAATATATTAATCCA 5385

QY 4995 gatggacttgcccatggtgatggggagccgcctccattgcatggatgttctcttctttt 5054
Db 5386 GATGGACCTGCGCTTGGTCCCGGGGATAAGATCCCACTCTCTGGACATCCTTTTGCCTT 5445
QY 5055 cactaccaggggtctctcgggactccagcgcttggtatccatgaaacacatgatggagga 5114
Db 5446 CACAAAGACGCTCTGGGAGAAATCCGGGAGTTGGACTCCTTGAAGACCAATATGAAGA 5505
QY 5115 gaagttatggaggcccaacccttttaagaagctctctacgagcccatagtcaccaccacaa 5174
Db 5506 GAAGTTTATGGGACCAATCTCTCCAAAGCATCTCTGAACCAATAGCCACCACCTCCG 5565
QY 5175 gaggaagaggaggaacaaaggcgccctcatccatccagagggcctaccggaacacatgga 5234
Db 5566 GTGGAAGCAGGAAGACCTCTCAGCCACAGTCAATTCAAAAGGCGCTACCGGAGCTACATGCT 5625
QY 5235 gaa 5237
Db 5626 GCA 5628

RESULT 2

US-08-843-417-9
Sequence 9, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5874 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-843-417-9

Query Match 23.5%; Score 1384.4; DB 4; Length 5874;
Best Local Similarity 57.3%; Pred. No. 0;
Matches 3227; Conservative 0; Mismatches 1926; Indels 477; Gaps 21;

Qy	58	aggtactaccggtgatcttccgcgacgagcggaatttccgcgccttcacttcgcactct	117
Db	1	ATGGAATTCCCATTTGGATGCTCGAAACTAACTTCCGCTTTTACTCCGGAGTCA	60
Qy	118	ctggctgccataaagaacggatctctatccaaaaggagagaagaagtcctcaagaacaag	177
Db	61	CTGGTGGAGATAGAGAAGCAAAATGCTGCCAAGCAGGGAACAAAGAAAGCCAGAGAAG	120
Qy	178	gc-----ggcagctgagcccgagcctcgctcagcttgacttaagggctcc	225
Db	121	CATAGGGAGCAGAGACCAAGNAGAGAAGCCTCGGCCAGCTGGACTTCAAAGCCTCG	180
Qy	226	agaaagttactaagctttatggtgacatcccccctgagcttgtaacgaacctctggag	285
Db	181	AACAGCTGCCCAAGTCTTATGCTGAGCTCCAGCAGAACTCATCGGGAGGCCCTGGAG	240
Qy	286	gacctgagccctactacaagaaccataagaacattcatgtgtgaacagaaaagaaca	345
Db	241	GATCTAGATCCGTTCTTACAGCACACACCGGACATTTATGGTGTGATGACAAAGGAGGAC	300
Qy	346	atttaccgtctcagcgccaagggcgcttcttcattctggggccttttaaccctcaga	405
Db	301	ATTTCGGGTTTAGTCCCACTCGGGCCCTGTGGCTATTACAGTCTTCAACCTGATCAGA	360
Qy	406	agcttaatgattcgtactctctgtcattcaagtccttagcatggttcaatcgcacgggtg	465
Db	361	AGAACGGCCATCAAACTGTCTTCACACTGTGGTTCAGTTATTTATTTACGGTTCATATT	420
Qy	466	atctcaactgtatgttcgatgcggaattctatggagagaagttcgcacaagacattccc	525
Db	421	TTGGTTAATGTGTGCAATGAC-----CCGAAGTGCCTTCAGAGAAAAATT	468
Qy	526	gaatacgtcttcattgggatttatattttagaagctgtgattaaaaatttggcaagggc	585
Db	469	GAATATGCTCTTACTGCTATTTACACCTTTGAAGCCTTGATAAGATACTGGCAAGAGGA	528
Qy	586	tcaatgtggatgagtttccctctcgcgagatccgtggaaactggctggacttcattgctc	645
Db	529	TTTTGTCTAAANGAGTTACAGTACCTGAGAGATCCTTGGAACTGGCTGGATTTTAGGCTC	588
Qy	646	attggaacagcgatcgcaactgtttccgggcagcccaagtcattcttcagctcttcgt	705
Db	589	ATTACCTTGCATATGTTGGCAGACAATAGATCTCCGTGGGA---TCTCAGGCGCTCGG	645
Qy	706	accttcagcgtctcagcgtctcgaaggcatttcagttatctcaggtctgaaggctcatc	765
Db	646	ACATTCAGAGTCTTTAGACGATTAATAACAGTTTTCTGTGATCCAGGCGCTGAAGGTCA	705
Qy	766	gtaggTgcctgctgcgctcggtgaagaagctggttagcgtgtagtggtccctcactctctc	825
Db	706	GTGGGGCCCTGATTCATCTAGTGAAGAAGTGGCTGATGTGACCATCTCTCACCATCTTC	765
Qy	826	tgctcageatctttgcccctggtcggtcagcagctgttcatctgggaattctgaaacagaag	885
Db	766	TGCTTAAGTGTCTTTTGGCTTGGTGGGCTGCAACTCTTCAAGGGCAACCTCAAAAATAA	825
Qy	886	tgattaaagcaaacctgtggcccaaacctgcattccaacaa-----g	927
Db	826	TGTGTCAAGAAATGACATGCTGTCAATGAGACAAACCACTACTCATCTACAGAAAAACCA	885
Qy	928	gattgctttgaaaggaaaaagatagcgaagacttcaatgtgtggtacctggctcgcc	987
Db	886	GATATCTACATAAATGAGCGAGGCATCTGTGACCCCTTACTGTGTGGCAATGTGATCTGAC	945
Qy	988	agcagaccctgtccccaatggttctactgctgcgataaaacccatgaacccagacaataat	1047
Db	946	TCAGGCCACTGCTGATGTTATATCTGCCTTAAACTTCTTGACAACCCGGATTTTAAC	1005
Qy	1048	tatacaaaagttgaaacatttggctggctcttctcggccatggttcccggttatagactcaa	1107
Db	1006	TACACACAGCTTTGATTTCTTCTTGGGCTTTCCCTCTCACTGTTCCCGCTCATGACACAG	1065

Cy	1108	gactcctggagagggtttaccagacaga	tcctctgcyggaacctctgggatactactt	gtcttc	116
Dp	1066	gattttctgggaacgcctctaccagcagac	ccctcttgagacttcttggaataatctat	atgac	1125
Qy	1168	ttcttgatggtgtaattcctgggtcctct	ctactcctgaacttaacctgaacctgctgt	1227	
Dp	1126	TTTTTTGGTCTCGTAATCTCTCTGGGAT	CTTCTTACCTGGTCACTTGATCTTGCGTGA	1185	
Qy	1228	gtcacatggcttatgaagaacacagaaatg	lagctgctgagacagagcccaaggag	1287	
Dp	1186	gtcaccatgscgtatgaggagcagAACAGCA	CCACTGATGAATTTGAAGCAAGGAG	1245	
Qy	1288	aaatgttccagaaagccccagcagctgtt	taaggaggagagggctctgtgttgcacatg	1347	
Dp	1246	AAGAAGTTCCAGGAGGCCCTCGAGATGCT	CCTCGGAAAGGAGCAGGAGGTGCTAGCAGCACTA	1305	
Qy	1348	ggaattgacagaagtcccttaattcctctta	ctccttaagcttcaactctttccccaagaa	1403	
Dp	1306	GGGATTGACACAACCTCTCTCCACTCCC	ACAATGGATCACCTTTAACCTCCAAAATGCC	1365	
Qy	1404	-----	-----	1403	
Dp	1366	AGTGAGAGAGGCATAGATAAGCCAAGCT	GTCTCAGAGGGCTCCACAGAGACACAACAA	1425	
Qy	1404	-----	-----	1403	
Dp	1426	TCACCCGGCTCTGATCCTTACAAACCAG	CAGCAGGATGTCTTTTCTAGGCGTCGCCCTCTGGA	1485	
Qy	1404	-----	-----	1403	
Dp	1486	AAAGCGCGGCTAGTCATGCGCAGTGTGT	TCCATTTCCCGTCCCTTGGCCGAGATATCTCA	1545	
Qy	1440	ctttatgagagggtccaaagcgg	-----	1462	
Dp	1546	CTCCTTGAGGAGTCACAGATGATGAGAT	CTTTCTTGAGACCACGAAAGCCATCGGGGC	1605	
Qy	1463	-----	-----	1464	
Dp	1606	TCCTCTGCTGGGTGGGGGTGCTGGCCAG	CAGAGGCCCTCCCTCTAGAAGCCCTCTTCCCT	1665	
Qy	1465	caagcctcaaggtctgattcagaggacgat	gctcctctaaaaatccaagctcc-----	1518	
Dp	1666	CAACCCAGCAACCTCTACTCCAGGCATG	GAGAAAGATGAACACCAACCGCCGCCACTAGT	1725	
Qy	1519	gagcagaccaaaacgactgtcccagaact	gtccagtggaatctctttgtagagca-----	1571	
Dp	1726	GAGCTGCCCTGGAGCTGTCGATGTCTCG	GCATTCGATGCAGGACAAAGAACACTTTC	1785	
Qy	1572	-----	-----	1614	
Dp	1786	TTGTGACGAGAATACTTAGATGAACCTT	TCCGGGCCCAAGGGCAATGAGTGTGTGAGT	1845	
Qy	1615	atcttaacatcaccatacagaaacaagaaa	aatctccaggagccttgtttcccatgtggg	1674	
Dp	1846	ATCATAACCTCCGCTCTGAGGAACTCG	AGGAGTCTGAACAAGATGCCACCCCTGCTTG	1905	
Qy	1675	aaaaattggcctctaagtacctgtgtggg	actgtagccctcagtgctgtgcataaag	1734	
Dp	1906	ACCAGCTTGTCTCAGAGATATCTGATCT	GGGATTCTGCCCCATCTGGGTCAAGCTCAAG	1965	
Qy	1735	aaggctctgcggaccatcatgacggaatcc	ctttactgagctggccatcaccatctgcatc	1794	
Dp	1966	ACAATTCTCTTTGGGCTTGTGAGGGAT	CCCTTTTGAGAGCTCACCATCTGTGTCATC	2025	
Qy	1795	atcatcaataccggtttcttagcgttggg	agacacacaatgga tgaacaacttaagaacc	1854	
Dp	2026	GTGTGTAAACCACTTCATTGGCCATG	GAGACCACTATGGCATTTGCGAAGCC	2085	
Qy	1855	atactgaaatagaaacctgggtttttcag	gaaatttcatagcggaaatgtgtcctcaag	1914	
Dp	2086	ATGCTCCAGATAGCAACATCGTCTTTAC	CAATTTTTTTTACTGCTGAAATGGCTTCAAA	2145	
Qy	1915	atcatgcgcgtcagaccttaccactactt	ccagcagcgcgtggaatgttttgcacagcatc	1974	

Db 2146 ATCATTGCCCTTCGACCATATCTATTTCAGAGAAGTGAATATCTTTGACTGCATC 2205
QY 1975 gtggccctcctgagtcctgctgctgctctacacacactgctgataacaataggtct 2034
Db 2206 ATCGTCACTGAGTCTGCTAGAGCTGGGGCTGGCCA-----AGAAAGGAAGCCTGTCT 2259
QY 2035 tcttggtctccctcagagctgagggctctcaagctagccaaactcgtgcccaggtta 2094
Db 2260 GTGCTGGGAGCTTCGCTTGCTGGCGTATTCAAGCTGGCCCAATCTCTGGCCCACTTA 2319
QY 2095 aacactctcattaagatcatcgccactcgtgggcgcttggaacactgactggtgc 2154
Db 2320 AACACACTCATCAAGATCATCGGAAACTCAGTGGGGCACTGGGGAACCTCACCATCATC 2379
QY 2155 ctgactatcggtctctcattctctctgctggtgggaatcggtctcttcggacacaaagttt 2214
Db 2380 CTGGCCATCATGCTTTGCTTTGCTGCTGTTGGCAAGCAGCTCTAGGGGAAAATAC 2439
QY 2215 aacaagaccgcctacgcccagcagcggcc-----caggcgcgctggcacatggat 2268
Db 2440 CGTAACMACCGAANAATATCTCGCGCCCATGAGACTTGGCCCGCTGGCACATGCAC 2499
QY 2269 aattctaccactcctctcctggtggtctccgcatcctctggtgggaatggtacgagaac 2328
Db 2500 GACTTCTCCACCTTTCTCCATGCTCTCCGATCTCTCTGAGAGTGGATGAGAAC 2559
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RESULT 3			
US-09-024-020B-1			
Sequence 1, Application US/09024020B			
Patent No. 6030810			
GENERAL INFORMATION:			
APPLICANT: DELGADO, STEPHEN G.			
APPLICANT: DIETRICH, PAUL S.			
APPLICANT: FISH, LINDA M.			
APPLICANT: HERMAN, RONALD C.			
APPLICANT: SANGAMESWARAN, LAKSHMI			
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE			
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICED VARIANT THEREOF			
NUMBER OF SEQUENCES: 43			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: JANET PAULINE CLARK			
STREET: 3401 HILLVIEW AVENUE, MS A2-250			
CITY: PALO ALTO			
STATE: CA			
COUNTRY: U.S.A.			
ZIP: 94304-1397			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/024,020B			
FILING DATE: 16-FEB-1998			
CLASSIFICATION: 536			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 60/039,447			
FILING DATE: 26-FEB-1997			
ATTORNEY/AGENT INFORMATION:			
NAME: CLARK, JANET P.			
REGISTRATION NUMBER: 34,799			
REFERENCE/DOCKET NUMBER: R0020B-REG			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (650) 852-3097			
TELEFAX: (650) 855-5322			
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 5977 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: DNA (genomic)			
US-09-024-020B-1			
Query Match 19.8%; Score 1168.4; DB 3; Length 5977;			
Best Local Similarity 60.3%; Pred. No. 8.2e-295;			
Matches 2225; Conservative 0; Mismatches 1346; Indels 119; Gaps			
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Db 4888 GGGCGCATCTTGGCTCTGATCAAGGGCCCAAGGGATCGCACCTGCTCTTTGCGCTTA 4947
Qy 4456 atgagtctctctctctctctctcaacatcggtctgtctctctctctctctctctctct 4515
Db 4948 ATGATGTCGTGCGCGCCCTGTTCAACATCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 5007
Qy 4516 taagccatctttggatgagctgtgttttccaaagtgaagggctcgggagatcagac 4575
Db 5008 TTCTCCATTTTGGCATGTCCAACCTTCGCATACGTGAAGCAGCAGCGCGCATTTGACGAC 5067
Qy 4576 atcttcaacttcagacaccttacgggcagcatgctgtgtctctctctcagataaacactcg 4635
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Qy 4636 gctggtgggataccctcctcctcaaccccatgctgga-----ggca 4674
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Qy 4735 tacttcaggttatcatcatctctctcctcctcctcctcctcctcctcctcctcctcctcct 4794
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Qy 4855 ttgaaatcttctatgaggtctgggagaaagtttgaccccgagcgctgcaggttcattccag 4914
Db 5368 TTCGAGACTTTCATGAGATCTGGGAGAACTTTGACCCACGACGACCCAGCTTCATCGAG 5427
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Query Match

19.8%; Score 1168.4; DB 3; Length 6007;

5428 TACTGTAACTGGCAGACTTTTCCGACGCCCTTGAGCAGCCCGCTCCGAGTAGTACCAAGCCC 5487
Qy 4975 aataagtttcagttcttagtgatgacttgcctcatggtgagtgggcgaccgctccattgc 5034
Db 5488 AACACCATCGAGCTATCGCCATCGACCTGCCATGTGTGAGCGAGATCGCATCCACTGC 5547
Qy 5035 atgagatctctcttcttctcactaccaggtctcctcgggactccagcggcttgatcc 5094
Db 5548 TTGACATCTCTTTTCGGCTTCCACCAAGCAGTCTCTGGAGACAGTGGGGAGTTGGACATC 5607
Qy 5095 ataaaaaccatgatgaggaagatttatgagagcccaaccttttaagaagctctcag 5154
Db 5608 CTGGCGGACAGATGAGGAGCGGTCTGTGCATCTCCATCTCCAAAGTCTCTTAGCAG 5667
Qy 5155 cccatagtcacccaccacccaaagagagagagagagagagagagagagagagagagag 5214
Db 5668 CCTATCACAACCACTCTCTGGCGCGCAAGCAGGAGGAGGTGTCTGCAGTGGTCTCGAGGT 5727
Qy 5215 gctaccggaacacatggaagaagatggtc 5244
Db 5728 GCCTACAGGGACACTTTGGCTAGCGGGGC 5757
RESULT 4
US-09-024-020B-2
Sequence 2, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6007 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-024-020B-2

Db 4198 GTTAACCTGTTGGGGGAATACCACACTACTGCTTTAATGAGACTTCTGAAATCCGGTTC 4257
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QY 4516 tacgcatctttggatgagctggtttccaaagtgaagaagggtcgcggatcgcagac 4575
Db 5155 TTCTCCATTTTGGCATGTCCAATCTCGCATAGTGAAGCACGAGCGCGCATTTGAGGAC 5214
QY 4576 atcttcaacttcagaccttcaggcagcagatgctgtcctctctcagaatacaactctg 4635
Db 5215 ATGTTCAACTTCGACATTTGGCAACAGCATGATGTTGTTTCCAGATCACAACGTCT 5274
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Db 5275 GCTGGCTGGATGGCTGTCTGCTGCTCAATCTGTAACCGCCCTCTGACTGAGCTTGGAC 5334
QY 4675 aaagaacactgcactcctcctcccaagacagctgtgcagcagcgcagatagccgtcgtc 4734
Db 5335 AAAGAGCACCCAGGAGTGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTC 5394
QY 4735 tacttgcagttacatcatct 4794
Db 5395 TTCTTTGTGAGCTACATCATCT 5454
QY 4795 atctcgaagacttcaacacagccacgagagagagagagagagagagagagagagagag 4854
Db 5455 ATCTTGAGAACTTCACGCTGGCCACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5514
QY 4855 ttgaaatctctctatgaggtctgggagaagtgttgacccccgagcgctgcgacttccatccag 4914
Db 5515 TTGAGACTTTCTATGAGATCTGGGAGAACTTTGACCCAGACGCCACCCAGTTTCATCGAG 5574
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Db 5695 TTGACATCTCTTTTGGCTTTCACCAAGCGAGTCTCTGGAGACAGTGGGGAGTTGGACATC 5754
QY 5095 atgaaacacatgatggagggagaggtttatggagggcaaccccttttaagaagctcagag 5154
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Db 5875 GCCTACAGGAGACACTTTGGCTAGGCGGGC 5904

RESULT 6.

US-09-024-020B-43

Sequence 43, Application US/09024020B

Patent No. 6030810

GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.

APPLICANT: DIETRICH, PAUL S.

APPLICANT: FISH, LINDA M.

APPLICANT: HERMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI

TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: JANET PAULINE CLARK

STREET: 3401 HILLVIEW AVENUE, MS A2-250

CITY: PALO ALTO

STATE: CA

COUNTRY: U.S.A.

ZIP: 94304-1397

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/024,020B

FILING DATE: 16-FEB-1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

Query Match	19.8%;	Score 1168.4;	DB 3;	Length 6586;
Best Local Similarity	60.3%;	Pred. No. 8.6e-295;		
Matches 2225;	Conservative	0;	Mismatches 1346;	Indels 119;
Gaps				
QY	1616	tcttaaacatcacccatcacaggacaagaataattccaggagccctgtttcccatgtggga	1675	
DB	2303	TCACAACACGCTAGTGGGAAGAGCTGGAAGAGTCTCAGAGAAAGTGCACCGTGTGCT	2362	
QY	1676	aaatttgcccttaagtagcttggtgggactgtagccctcagtcgctgtgcataaaga	1735	
DB	2363	ATAAGTTTGGCAACACTTTCCCTCATCTGGGAGTGTCACCCCTACTGTGATAAACTGAAGG	2422	
QY	1736	aggctctcgggaccatcatgacgagtcaccttttactgagctggccatcaccatctgcatca	1795	
DB	2423	AGATCGTAACCTTAATCGTCATGGACCCTTTTGTGTAGACTTAGCCATCACCATCTGCATCG	2482	
QY	1796	tcatcaataaccgctttcttagcgtggagcaccacaacatgtagcaactttaaagacca	1855	
DB	2483	TTCTGAATACGCTATTATATGGCAATGGAGACCATCCCATGACACCACAGTTCGAACACG	2542	
QY	1856	tactgaaatagaaaactgggtttttcacgggaattttcatagcggaaatgtgtctcaaga	1915	
DB	2543	TCPTGGCCGTAGGAATCTGGTGTTCACCGGGATCTTCACGGCGGAATGTTTCTGAAGC	2602	
QY	1916	tcatcgctctgacaccttaccactacttccggcagcgctggaatgtttttgacagacatcg	1975	
DB	2603	TCATAGCCATGNAACCCCTACTATTATTTCCAGAAGGCTGGAAACATTTTTCACGGATTTA	2662	
QY	1976	tggccctcctgagctcgcgtgtgctctacaacacactgctctgataacaataggtctt	2035	
DB	2663	TTGCTCTCCCTCAGTTTAAATGGAGCTGAGTCTCGCAGATGTGGAGGGGCTC-----TCAG	2716	
QY	2036	tcttgctctcctcagagtgctgaagggtcttcaagttagcacaatactgcccacgttaa	2095	
DB	2717	TGCTGCGGCTTTTCCGACATGCTCCGAGTCTTCAAGCTGGCCAAAGTCTCTGGCCACCGCTGA	2776	
QY	2096	acactctattaagatcatcgccactcgtgggcgctgtggaacctgaactgaactgtgttc	2155	
DB	2777	ACATGCTGATCAGATCATCGGGAACCTCGTGGTGGCCCTGGGCAACTGACCCCTGGTGC	2836	
QY	2156	tgactatcgtgttcttcatctttctgtgtgggcgcatcgccctctcggcaccacgttta	2215	
DB	2837	TGGCCATCATCTGCTTTCATCTTCGCCGTGGTGGGATGTCAGCTCTTTGGAAAGAGTTTACA	2896	
QY	2216	acaagaccgcct---acgcccacccaggagcgccacagcgcgctgcacatggataatt	2272	
DB	2897	AGGAGTGCCTCTCTAAGATCAACACAGAGTAGTCAAGCTCCCGCGCTGGCAGCATGAACGACT	2956	
QY	2273	tctaccactctctcgtgtgtgttccgcatactctctgtggggaatgaatcgagaaacatgt	2332	
DB	2957	TCCTCCACTCCCTTCTCATCTGCTTTCAGAGTGTGTGTGGGGAATGATCGAGACCATGT	3016	
QY	2333	ggggctgcatgcagatattggacggcgtcccccgtgtgtgcatcatgtcttcttcctgataa	2392	

Qy	2698	ttgtacactggacagcgccggggtccgcgtgcccccaactcgcagaggtagaggaacgatactgt	2755
Db	3175	AAGGAAAAAGATAAAAATCAAGTCAGTTGGTGGAAAGCAGCGTGGACAACACTTGTATGGAAGAC	3234
Qy	2758	gaatattgtgtgaagcggtgccctaccccaacctcaaacatagtcgtggaattcagagcc	2817
Db	3235	AGTGATGGTCAATCATTTATTCACAATCCAGCCCTCACAGTGACAGTGCCAATTTGCACCT	3294
Qy	2818	ggtgacctccctccagagaccaagcagctcactagccgcggtaccacaaagggttggaaatg	2877
Db	3295	GGGGAATCCGATTTGGAAATATGAA-----TGCTGAG	3327
Qy	2878	gaagtatttctgaagaagatctgcattttaagcaacacagagtcctcgaagaagctctgac	2937
Db	3328	GAACCTAGCAGTATTCCGATAGTGAATACAGACAAGTGAGATTAAACCGGTCAAGCTCC	3387
Qy	2938	gcagtgaagatgctctcggaattgcagcacaaattgacctgaatgatatctttagaataatta	2997
Db	3388	TCAGATGACA-----GCACAGTTGATAACCCCTTTCCTCGGAGAGGAGAGAAGACGAGG	3448
Qy	2998	cagaaaaacagttccccccaaaaagcagccagatagatctttcccaaggcccttagttgt	3057
Db	3443	CTGAACCTATGAATCCGAT---GAGCCAGAGGCGCTGTTTCACAGATGGTGTGTACGG	3498
Qy	3058	caactttctatgccccaaaaacagacaagaagaaagtcctccctgggtctctgtgtggaacatt	3117
Db	3499	AGGTTCTCATGCTCGCCAAAGTTAACATAGATGACGGAAAGGAAAAAATCTGCTGGAACATC	3558
Qy	3118	cggaaaaactgtaccaaactcgtgaagcacagctggtttgagagtttcaataactttgtt	3177
Db	3559	AGGAAAACCTGCTACAAAGATTTGTTGAACACAGTGGTGTGAAAGCTTCATTTGCTCATG	3618
Qy	3178	attctgctgagcagtgagcgctgataatttgaagatgcaactctcccagcgcgcacaa	3237
Db	3619	ATCCTGCTCAGCAGTGGTCCCTGGCTTTGAAGATATTTATATTGAAGGAAAAAAGACC	3678
Qy	3238	gttgagaaattactaagggtgtaaccgataataatttccacattatttctctctgtggaatg	3297
Db	3679	ATTAAAGATTATCTGGAGTATGCAGACAAGATCTTCACTTACATCTTCATTCTGGAATG	3738
Qy	3298	atctggaagtggtgaccttggattccggaagttattccacagtcgctggtactgacctt	3357
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Qy	3358	gatttctcatgttggtggtgctgtgctgctcagctccatg-----	3396
Db	3799	GATTTCTTAATTTGTTGATGTTCTTTGGTTACTTTAGTGGCAACACACTTTGGCTACTCA	3858
Qy	3397	aatctaccaagcttgaagtccttcgcgactctgcggccctgagacctctgcgggcgctg	3456
Db	3859	GATCTTGGCCCCATTAATCCCTTCGGACACTGAGAGCTTAAGACCTCTAAGAGCCTTA	3918
Qy	3457	tcccagtttgaagaagaatgaagttgtcgtctacgacctgatcagcgccaacctgcacct	3516
Db	3919	TCTAGATTTGAAGGAATGAGGTCGTTGGAATGACACTCATAGGAGCAATTTCTTTCATC	3978
Qy	3517	ctcaattgtctgtgctgctgcctcatcttctgctcgctattttgtattcttggagtaaat	3576
Db	3979	ATGAATGTGCTACTTCTGTGTCTTATATCTGGCTGATATTTCAGCATCATGGGAGTAAT	4038
Qy	3577	ttatttctgggaagtttggaaagtgcatctaacgggacagacataataatgtatttggat	3636
Db	4039	TTGTTTCTGGCAAGTTCTATGAGTGTATTAAACACCACAGATGGCTCAGCG---TTTCTCT	4095
Qy	3637	ttaccgaagttccgaacccaagcaaatg-----taacattagtaatactac	3681
Db	4096	GCAAGTCAAGTGTCCAATCGTTCCGAATGTTTTGGCCCTTATGAATGTGTAGTCAAAATGTG	4155
Qy	3682	tctgtgaaggtcccgagctcaactttgacaacgtggggaatgcctatctcgccctgctg	3741
Db	4156	CGATGGAAAAACCTGAAAGTGAACTTTGATAATGTGGACGTTGTTTACCTATCTCTGCTT	4215
Qy	3742	caagttggcaacctataagggtggtcggtggaatacaatgaatgctgctgtcgaattccagagag	3801

4216	CAAGTTGCAACTTTTAAAGGATGGACGATTATTTATGTATGCAGCAGTGCGATTCTGTAAT	4275
3802	aagacgacgcgcggactttgaggcgaaacctctcagcgatctctactcttctgttgtttt	3861
4276	GTAGACAAGCAGCCCAAATATGAATATAGGCTCTACATGATATTTATTTTTGTGCTGTTT	4335
3862	atcatcttcggctctctctttaccctgaacctctttatcggttgtttatattgacaacctc	3921
4336	ATCATCTTTGGTCATCTTCACCTTTGAACTTGTTCAATTGGTGTCTCATCATAGATAATTTC	4395
3922	aatcagccgcgaaaaagttagtggccaagaacatttttatgacagaagaacagaaa	3981
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4456	TACTATATGCAATGAAAAAGCTGGGGTCCAAGAGCCACAAAAGCCAAATTTCTTCGACCA	4515
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4756	TTTGTATTTTGTGGTTGCAATTATCTCCATTGTAGGTATGTTTCTAGCTGATTGTATTGAA	4815
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4462	tctctcccctctctttaaactatgctgtgctctctcttggtgatgttcattacgcc	4521
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Db 5293 CTGAGAGAAATTTAGTGTGGCCACTGAAGAAGTACTGAACCTCTGACTGAGGATGACTTT 5352
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Qy 5218 ta 5219
Db 5713 TA 5714

RESULT 10
US-08-836-325-14
Sequence 14, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Haleboua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA: 08/482,401
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0917.0240002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 6404 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-836-325-14
Query Match 17.3%; Score 1017.6; DB 3: Length 6404;
Best Local Similarity 57.8%; Pred. No. 2e-255;
Matches 2143; Conservative 0; Mismatches 1459; Indels 120; Gaps 13;
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/338,702
; FILING DATE:
;
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen III, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 1938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
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; US-08-338-702-7
;
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Best Local Similarity 52.16%; Pred. No. 2e-166;
Matches 1941; Conservative 0; Mismatches 1569; Indels 183; Gaps

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Qy 4435 aggacctcctcttctgttggatgatgtctctccctctctctcttcaaacatcggtctctg 4494
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Dy 5331 CTGTTCTGCTGCTATGTTTCATCTTTGCGCATTTTTCGCTGCTCTTTCATCATGACGCTGAAG 5390
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Dy 6045 CTAATCAGCAGCCTGGCGAAAGCACAAAGCGC 6077

RESULT 14

US-08-337-339-7

Sequence 7, Application US/08337339

Patent No. 5593864

GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

APPLICANT: Hall, Linda

APPLICANT: Feng, Gouping

APPLICANT: Van Der Ploeg, Leonardus

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

TITLE OF INVENTION: PARA SODIUM CHANNEL

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESSES:

ADDRESSEE: John W. Wallen III

STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CITY: New York, New York

STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,339
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19332
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-337-339-7

Query Match 11.5%; Score 676.6; DB 1; Length 6513;
Best Local Similarity 52.6%; Pred. No. 2e-166;
Matches 1941; Conservative 0; Mismatches 1569; Indels 183; Gaps 14;

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Db 5391 GAGAAGAGCGCATTAACGAGGTCTACAACCTTCAAGACCTTTTGGCCAGAGCATGCTCG 5450
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Db 5985 GAGGCTACGAGCCGCTCTCATCAACGCTGTGGCTGAGCGTGTGAGGAGTACTGCGCGCGG 6044
Qy 5203 gtcacacagagggcctaccggaacacacatgag 5235
Db 6045 CTAATCAGCAGCGCTGGCGAAAGCACAAAGCG 6077

RESULT 15

US-08-724-095-7

Sequence 7, Application US/08724095

Patent No. 5688917

GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

APPLICANT: Hall, Linda

APPLICANT: Feng, Gouping

APPLICANT: Van Der Ploeg, Leonardus

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

TITLE OF INVENTION: PARA SODIUM CHANNEL
NUMBER OF SEQUENCE: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand - Merck & Co., Inc.
STREET: P.O. Box 2000 - 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTseq. Version #1.d5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,095
FILING DATE:

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19332DA
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-08-724-095-7

Query Match 11.5%; Score 676.6; DB 1; Length 6513;
Best Local Similarity 52.6%; Pred. No. 2e-166;
Matches 1941; Conservative 0; Mismatches 1569; Indels 183; Gaps 14;

QY 1699 gtgtgggactgtagcctcagtgctgtgcataaagaagtgctcgggacccatcagc 1758
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DB 2412 GTGTGGGAGCTGTGCTGGGTTTGGTGAATTTTCAGAGTGGGTATCGCTCGTCTTC 2471
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QY 2465 aggatggagccttggagggagagaccaggaacacaaaglgcagctagcctggatcggt 2524
DB 3180 GCCGATAACGATACGAATAAATAGCCGAGCCCTTCAATCGAATGGCCGATTTAAAGT 3239
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DB 3240 TGGGTTAAGCGTAATATTGCTGATTGTTTCAAGTTAATACGTAACAAATTTGACAAATCAA 3299
QY 2585 ggaggaaaaactcgcaaaagccaaagagacacacagaaaagccttcttcttcttcttctt 2641
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QY 2642 -----aagactcaatcctcccgagctcgcgagcctcgagcctcg 2673
DB 3360 CATGGTGACAACGAACGTGGAGCTGGGCCACGACGAGATCCTCGCCGACGGCTCATCAAG 3419
QY 2674 aaggagtatgatacagacatggcttg-----t 2701
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QY 2821 gacctcctccagagacacagcagctcactagcccggtgaccaaaggggttgaaatgaa 2880
DB 3600 GGTGTTGTCTTACAGGACGACGACACTGCCAGCATTAACCTCATATGCTAGCCATAAGAAT 3659
QY 2881 gtatttctgaagaagatctgca-----ttaagcat 2912
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QY 2913 acagagtccttcgaagaagtctgacgagtgagcatgctctcgtgaaatgcagacaaattga 2972
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QY 2973 cctgaa-----tgatatctttagaataattacagaaaaacagtttcccccaaa 3018
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DB 3900 GACGATGACTCGCGCTTCTGCAAGGATGGGCAATTTACGACTGAAACTTTTCAATTA 3959
QY 3139 gtaagcacagcgtggttggagagtttcaataatttcttcttcttcttcttcttcttcttctt 3198
DB 3960 ATTGAAATAAATTTTGAACAGCTGTTTATCACTATGATTTTAAATGAGTAGCTTAGCT 4019

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 17:49:55 ; Search time 5057.4 Seconds
(without alignments)
12529.730 Million cell updates/sec

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Sequence: 1 gtagcaccatcggtgcctga.....gaaaaaaaaaaaaaaaaaaaaa 5897

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
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5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_estl:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541.2	9.2	650	11	BG694370 NISC_iv01
2	485.4	8.2	892	11	BF980111 602288113
3	305.4	5.2	778	10	AU035605 AU035605
4	283.4	4.8	615	10	AW133907 AW133907
5	266.6	4.5	674	11	BG342331 602374246
6	255.4	4.3	690	10	BE550573 7a29e10.x
7	247.8	4.2	561	11	BF076296 225823 MA
8	243.2	4.1	619	13	Z86536 F.rubripes
9	239.6	4.1	610	10	AL588672 AL588672
10	236.6	4.0	689	11	BF347024 602021819
11	236.2	4.0	779	10	AU051532 AU051532
12	234.2	4.0	529	10	AA183990 ms53e02.r

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14	226.4	3.8	518	11	BG578677 dac36c11.
15	220.8	3.7	501	13	CNS04HC1
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17	217.8	3.7	544	11	BF323267 maa38e08.
18	211.4	3.6	668	13	AZ438465
19	207.6	3.5	675	13	AZ960529 2M0228C09
20	207.4	3.5	731	10	AI796228 wh44d06.x
21	205.4	3.5	438	13	AZ495334 1M0331P08
22	193.8	3.3	330	10	AA913881 om21h12.s
23	193.8	3.3	435	10	AA885211 am34c11.s
24	193	3.3	662	11	BG253038 602365660
25	192.6	3.3	902	11	BG761119 60217452
26	192.4	3.3	441	11	BE864903
27	188.2	3.2	721	13	BH035847 RPCI-24-3
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29	179.6	3.0	566	13	AZ015753 RPCI-23-3
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31	176.2	3.0	934	10	AL517958
32	175.6	3.0	450	10	AL120392 DKF2P761E
33	174.4	3.0	457	10	AW159460 za99e07.x
34	173.4	2.9	437	10	AW495598
35	172.4	2.9	632	10	AJ396135
36	172	2.9	392	10	AW046964
37	169.4	2.9	951	10	AL533359
38	168.6	2.9	547	10	BE724185
39	167.6	2.8	343	11	F07776
40	166	2.8	540	10	BE121161
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42	163.8	2.8	812	11	BG666779 DRABWE08
43	161.4	2.7	521	13	AZ392948 1M0155J16
44	160.8	2.7	656	10	AV721039
45	160.2	2.7	399	10	AW771930 hn66f12.x

ALIGNMENTS

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LOCUS NISC_iv01b10.w2 Soares NMMP2 pituitary Mus musculus cDNA clone
DEFINITION IMAGE:4316490 5', mRNA sequence.
ACCESSION BG694370
VERSION BG694370.1 GI:13953218
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 650)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
MG1:1597258
Seq primer: T7 primer.
Plate: LLAM9919 row: C column: 19
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/db_xref="taxon:10090"
/clone="IMAGE:4316490"
/clone_lib="Soares NMMP2 pituitary"

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Best Local Similarity 89.5%; Pred. No. 3.7e-100;
Matches 582; Conservative 0; Mismatches 68; Indels 0;

FEATURES	source
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High quality sequence stop: 729.	
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/clone_lib="NIH_MGC_97"	
/lab_host="DH10B"	
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carinci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."	
207 a 213 c 214 g 258 t	
EASE COUNT	
ORIGIN	

Query Match	8.2%	Score 485.4;	DB 11;	Length 892;
Best Local Similarity	81.7%;	Pred. No. 8.5e-89;		
Matches 609;	Conservative 0;	Mismatches 131;	Indels 5;	Gaps 4;
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750	CCAGATCTTTGGGAGAGCCTTATCAACAGAACTCGGTA-CTACGGGCTCTACTCAGTC	692		
pb				
1165	ttcttcttggtgggtcatct-tcctgggtcctcttacctgccttaacctaaacctggc	1223		
pb				
691	TTCTTCTTCATTTGGTGCATTTGTCTGGGTCCACTACCTGATTAACT--TAACCTGGC	634		
pb				
1224	tggtgcacataggcttatgaagaacagacagaaaaatgtagctgctgagacagaggccaa	1293		
pb				
633	TGTTGTTTACCATGGCATATCAGGAGCAGACAAAGATGTAGCTCAGAGATAGAGGCCAA	574		
pb				
1284	ggagaaaattcttcaggaagccagagctgttaaggaggagagagagctctcggtgc	1343		
pb				
573	GGAAGAGATCTTTCAGGAAGCCCAGCAGCTGTTAAAGGAGGAAAGGAGGCTCTGGTTGC	514		
pb				
1344	catgggaattgcagagaagttcccttaattcccttcacagcttcaccttttcccagaagaa	1403		
pb				
513	CATGGGAATTTGACAGAAGTTTCATCTACCTTCCTTTGAACACATCATATTTTATCCCAAAAAA	454		
pb				
1404	gaggaagtttttcggtagtaagacaagaagctcctcttatagagaggttccaagacgac	1463		
pb				
453	GACAAAGCTCTTTGGTAAATAGAAAAGGAAGTCCCTCTTTTGTAGAGAGTCTGGGAAGA	394		
pb				
1464	ccaagctcagctgctgattcagaggacga-tgcctctaaaaatccacagctccttgagc	1522		
pb				
393	CCAGCTCTCTGGGTGCAGATTTCTGATGAAGATTGCCAAAAAAGCCACAGCTCTCTAGAGC	334		
pb				

REFERENCE 1 (bases 1 to 615)
 AUTHORS Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Stepien,M., Underwood,K., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.
 TITLE WashU Zebrafish EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: fl13c05.xl
 Contact: S.L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
 Sequencing by: Washington University Genome Sequencing Center
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 467.
 Location/Qualifiers
 1. .615
 /organism="Danio rerio"
 /strain="AB"
 /db_xref="taxon:7955"
 /clone_lib="Sugano Kawakami zebrafish DRA"
 /sex="mixed (one male and one female, including unfertilized eggs)"
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 /lab_host="DH10B (phage resistant)"
 /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGATG); Site_2: DraIII (CAGCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGTGGCTACTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGATG, 3' site CAGCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGTGGC and 3' end primer CGACCTGCGAGTCGACACA."
 BASE COUNT 155 a 156 c 158 g 146 t
 ORIGIN

Query Match 4.8%; Score 283.4; DB 10; Length 615;
 Best Local Similarity 67.3%; Pred. No. 1.9e-47;
 Matches 414; Conservative 0; Mismatches 196; Indels 3; Gaps 1;
 QY 3535 tgcctctattctgctcgtatttctggtgagtaattatttctggaagt 3594
 Db 2 TGCTGATCTTCGGCTCACTTCAGCATTTATGGGGTCAATCTGCTGGTGAAGTTT 61
 QY 3595 ggaaggtgcattaacgggagaca---cataaataatgtattgtatttaccgaagttccg 3651
 Db 62 GGCGCTGCGTGAACCGGCGGGTTTCATATAATCTCTGACATCAACAACCGCAGC 121
 QY 3652 aaccgaagcaatgaataactagtaattactgtggaaggtcccgaggtcaactttgac 3711
 Db 122 GAGTGTCTGGAGATGAACACGACGACGAGTATTACTGGACCAAAAGTAAATTTCCGAC 181
 QY 3712 aacgtggggaatgctatctcgccctgctgaagtgcacactataagggctgctgaa 3771
 Db 182 AACGTGGCGCTGGATATCTCGCGCTGCTGCAAGTGGCCACGTTTAAGGCGTGGATGGAG 241
 QY 3772 atcatgaatgctgctgattccagagagagacagcagcgacttttgaggcaac 3831
 Db 242 ATCATGTACCGCGCTGGAGCTCGAGAGCTGTGGAGGACCAACCAATCAAGGAAACAGC 301
 QY 3832 ctctacgcgtatctctactttgtggtttttatcatctctcggtctctcttaccctgaac 3891
 Db 302 CTGTACATGTACCTGATCTTCGTCATCTTCATCTCTCGGCTCCTCTTTTACCCCTCAAC 361

QY 3892 cctttatcggtgtattattgacaacttcaatcagcagcagaaaaagttaggtggccaa 3951
 Db 362 CTGTTCATCGGTGTGATCATCGCAACTTCAACGACGAGAGAGTATAGGGGGCAG 421
 QY 3952 gacattttatgacagagaacagaataattacaaatgcaatgaaagttaggaacc 4011
 Db 422 GACATCTTCATGACCGAGAGAGAGAATACTACACGCCCATGAGAAACTGGGCTCC 481
 QY 4012 aagaaacctcaaaagcccatcccaagccctgaacaaatgtcaagcctttgtgtgcac 4071
 Db 482 AAGAAGCACAGAGAGCCATACACGACACCAACCTGTCAGGGCTCTCTTCTTCGAC 541
 QY 4072 ctggtcacagccaggtctttgacgtcatcattctggtgttattgtcttaaatatgatt 4131
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 QY 4132 atcatgaggtcg 4144
 Db 602 ACGATGGATGGTG 614
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 LOCUS 602374246F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5',
 DEFINITION mRNA sequence.
 ACCESSION BG342331
 VERSION BG342331.1 GI:13148769
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-femail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAMI0317 row: 1 column: 12
 High quality sequence stop: 672.
 Location/Qualifiers
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 /note="Organ: eye; vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
 BASE COUNT 146 a 167 c 161 g 200 t
 ORIGIN

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 Best Local Similarity 65.6%; Pred. No. 3.9e-44;
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 QY 4061 ttgtgttcgacctggtcacagccaggtctttgacgtcatcttctggtgtttattgtct 4120
 Db 5 TGGTTTTTGACTTTGTAACCAAGCAAGTGTGTGATATACGATCATGATCATCTCATCTGTC 64

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D 65 TGAACATGTTGACATGATGGTGAAGAACGATGACACGAGCGATTATGTACACAGCATTT 124
QY 4181 ttgatatctcaacatagctcttgctgctcattcttaccatagagtgtctcacaagtct 4240
D 125 TGTACGCGATCAACCTGGTGTCTCTGCTGTTCCCGGAGCTGTGCTCAAGCTCA 184
QY 4241 ttgctttgaggcaactactcaccatggctgggaactatttattgttggctgtggtg 4300
D 185 TCTCGCTCGCCATTTATTTACCATTTGGATGGAAACATTTTCGATTTTGTGTTGTC 244
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QY 4361 ccaagctcttcagagctgctcgttggctgctgattggtgaattcctcaggctggtc 4420
D 302 CTACCTCTTTCGAGGATCCCGCTGGCAGGATTTGGACGAATCTTACGCTGTATCAAA 361
QY 4421 ctgcccggggaatcaggacctctcttctgcttgatgctctcctccctctctcttca 4480
D 362 GTCCCAAGGGATCCCGACGCTGCTCTTGTCTGTATGATGCTCCCTCTCGCTGTTTA 421
QY 4481 acatcggtctgctctctctctggtgctgttcttaccgcatcttgggagtgagctggt 4540
D 422 ACATCGGCTCCTGCTCTTCTGCTCATGTTTCATCTACGCCATCTTTGGGATGTCAC 481
QY 4541 ttctccaaagtgaagaaggctcgggagtcagacagacattctcaactcggagaccttac 4600
D 482 TTCCCTATGTTTAAGAGGGAAGTTGGGATTTGATGACATGTTTCAACTTTGAGACCT 541
QY 4601 gcaagctgctgctcctctccagataaccacttcgctgctggtgagataccctcctca 4660
D 542 ACAGCATGATCTCCCTGTTTCCAAATCACCACCTCTCGGGCTGGGATGAGTCTGTC 601
QY 4661 ccatgctgagggcaaaa 4677
D 602 CCATCTCAAAAGGAAA 618

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DEFINITION
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NAN...; mRNA sequence.
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VERSION BE550573.1 GI:9792265
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SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 690)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 456.
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FEATURES

source

Location/Qualifiers

1..690

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/db_xref="taxon:9606"

/clone="IMAGE:3220170"

/clone_lib="NCI-CGAP_G66"

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/lab_host="DH10B"

note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1; Not 1; Site 2; Eco RI; Plasmid DNA from the normalized library NCI-CGAP_G64 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 180 a 151 c 160 g 199 t

ORIGIN

Query Match 4.3%; Score 255.4; DB 10; Length 690;

Best Local Similarity 80.8%; Pred. No. 7.5e-42;

Matches 298; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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QY 1569 gcacgtggacccctccacaggcagagagcgtgagcgtgctcagtgatcttaaccatcac 1628

D 351 GCATGGAGATCTCTCCAAAGGAGAGAGCACTGCTGCTCAGCATCTCCACCATCAC 292

QY 1629 catacaggaaacaaattccaggagcctgtttcccatgtgggaaaaatttggcctc 1688

D 291 CATGAGGAACACAGAAATATCAAGAGACCTTGTCTCCCTTGGGAGAAACCTGGCATC 232

QY 1689 taagtacctgtgtggtgactgtagcctcagtgctgtgcataaagaagctcctgcggac 1748

D 231 CAAGTACCTGTGTGGAACCTGTGCCCCAGTGTGCTGCTGCTTAAGAGGCTCTGAGAAC 172

QY 1749 catcatgaaggatccctttactgagctggccatcaccatctgcatcatcatcaatccgt 1808

D 171 TGTGATGACTGACCCGCTTTACTGAGTGGCCATCACCATGTGCATCATCATCAACACTGT 112

QY 1809 ttcttagcgtgagac 1868

D 111 CTGTGTTGGCCATGGAGCATCAAGATGGAGGCCAGTGTGTTGAGAAGATGTTGAATATAGG 52

QY 1869 aaactgggt 1877

D 51 GAATTTGGT 43

RESULT 7

BF076296

LOCUS

BF076296 561 bp mRNA EST 25-APR-2001

DEFINITION

225823 MARC 280V Bos taurus cDNA 5', mRNA sequence.

ACCESSION

BF076296

VERSION

BF076296.1 GI:10869999

KEYWORDS

EST.

SOURCE

Bos taurus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 561)

REFERENCE

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrnkruug, S., Bennett

, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,

Petea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and

Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

RESULT 15

CNS04HCL/c

LOCUS

DEFINITION

CNS04HCL 501 bp DNA GSS 21-MAY-2000

Tetraodon nigroviridis genome survey sequence T7 end of clone
110M19 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

AL290746.1

VERSION

GI:8029326

KEYWORDS

GSS: genome survey sequence.

SOURCE

Tetraodon nigroviridis.

ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE

1 (bases 1 to 501)

AUTHORS

Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.

TITLE

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 501)

AUTHORS

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

TITLE

Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence

JOURNAL

Unpublished

REFERENCE

3 (bases 1 to 501)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

COMMENT

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

source

1..501

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone_lib="G"

/notes="Genoscope sequence ID : COBG110AG10LPL-end : T7"

94 a 133 c 116 g 133 t 25 others

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 67.2%; Score 220.8; DB 13; Length 501;

Matches 317; Conservative 15; Mismatches 138; Indels 2; Gaps 2;

Qy 4689 ctctctcccaagacagctgtcagcagccgagatagcgtctactctcgtcagttta 4748

Dy 473 CACCACCGTCAGGGGCAACTCGGGGACCCCGTGGGCGATCACCTCTTCGTMACGTA 414

Qy 4749 catcatcatctctctctcatcgttggtcaacatgtacatcgtgtgatctcgcgagaactt 4808

Dy 413 CATCATCATCTCTCTTTCTTATCTGTTGTTCAACATGATCGCCCATCATCTCGGAGAACTT 354

Qy 4809 caacacagc-cacgagagagagagagaccctctggagagagagactttgaaatctctt 4867

Dy 353 MAGCGTGGCAACCGAGGAGAGACCGAGCTCTGAGGGAGAGAGATTTCGAGATGTTCT 294

Qy 4868 atgaggtctggagaagtttgaaccccgagcgtcgcagttcattcgcgcctct 4927

Dy 293 ACAGAGTGTGGGAGAAGTTMGACCCGGAGGCAACGACAGTTAATDAGGTACGCCAAGCTGT 234

Qy 4928 ctgaacttggagagccctccgagcgttgctgtggccaaagcgaataagtttcagt 4987

Dy 233 CGGACTTCGCCGACTCTCTGTGGGAMMG-TGCGCATCGCVAAACCCMAAAAGATAAAGC 175

Qy 4988 ttctagtgtgagacttgcccatggtgatggcgacccgctccattgcattgattctct 5047

Dy 174 TGATCTCCAKGACMTGCCMATGCTMACTGGGGAMAAGATMMACTGCCTGGACATMATCT 115

Qy 5048 ttgctttcactaccagggtctctcgggactccagcgcttggataccatgaaaccatga 5107

Dy 114 TTGCMTTTCAMAAAGAGCGTTCATGGGCGAGTCCGGAGAGATGAACGAGYTCAGMAGAAGA 55

Qy 5108 tggagggagagtttatgtgagggcccaacccttttaagaagctctacgagcccat 5159

Dy 54 TGGAGGAGAAGTTTCATGATGCGCCCAACCCCTCAAAGATATWCATAGAGCCAAT 3

Search completed: February 26, 2002, 20:07:03

Job time: 8228 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2002, 22:39:30 ; Search time 76.96 Seconds
(without alignments)
1698.796 Million cell updates/sec

Title: US-09-646-224A-2
Perfect score: 9173
Sequence: 1 MEERYPIVFDERNFRFT.....VFCNGDLSLDVAKVYVND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : A_Geneseq_1101.*
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 - 2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT.*
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 - 13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9173	100.0	1765	AAV41668	Rat sensory neuron
2	9153	99.8	1765	AAV16572	Type 5 sodium chan
3	9149	99.7	1765	AAV06596	Rat sodium channel
4	9149	99.7	1765	AAH20122	Rat sodium channel
5	9141	99.7	1765	AAH20123	Rat sodium channel
6	8153	88.9	1765	AAV06597	Mouse sodium chann
7	8153	88.9	1765	AAH20124	Mouse sodium chann
8	6709	73.1	1791	AAH20121	Human sodium chann
9	4712.5	51.4	2016	AAW23594	Human hhl sodium c
10	4712	51.4	2015	AAH82242	Human SCN5A mutant
11	4711.5	51.4	2016	AAH82239	Human SCN5A protei

12	4711.5	51.4	2016	22	AAH82240	Human SCN5A mutant
13	4711.5	51.4	2016	22	AAH82245	Human SCN5A mutant
14	4708.5	51.3	2016	22	AAH82241	Human SCN5A mutant
15	4708.5	51.3	2016	22	AAH82244	Human SCN5A mutant
16	4704.5	51.3	2016	22	AAH82243	Human SCN5A mutant
17	4671	50.9	2020	11	AAH06584	Cardiac sodium cha
18	4669.5	50.9	1956	22	AAH61996	Human peripheral n
19	4663	50.8	2019	16	AAH67913	Cardiac sodium cha
20	454.5	49.7	1957	18	AAW21740	Variant rat DRG (S
21	4553	49.6	1956	22	AAH61995	Rat peripheral ner
22	4541.5	49.5	1957	18	AAW21737	Wild type rat DRG
23	4541	49.5	1977	17	AAH99641	Peripheral nervous
24	4518	49.3	1962	20	AAV17250	NaNg polypeptide.
25	4513.5	49.2	1243	22	AAH20136	Human sodium chann
26	4513.5	49.2	1984	17	AAH99639	Peripheral nervous
27	4510.5	49.2	1243	20	AAV06598	Human sodium chann
28	4506	49.1	2005	22	AAH99677	Human neonatal for
29	4505	49.1	2005	22	AAH99676	Human adult form o
30	4500.5	49.1	1989	17	AAH92317	Peripheral nervous
31	4496	49.0	2009	22	AAH99674	Human adult form o
32	4480	48.8	2132	18	AAW21739	Variant rat DRG (S
33	4470.5	48.7	1951	22	AAH99679	Human neonatal for
34	4468.5	48.7	1233	22	AAH20125	Human sodium chann
35	4466.5	48.7	1951	22	AAH99678	Human adult form o
36	4394.5	47.9	1978	19	AAH69361	Tetrodotoxin-sensi
37	4390.5	47.9	1988	19	AAH99640	Tetrodotoxin-sensi
38	4390.5	47.9	1989	17	AAH99640	Peripheral nervous
39	4354	47.5	1980	21	AAH23563	Human sodium chann
40	4195	45.7	1835	17	AAH92316	Peripheral nervous
41	3554.5	38.7	2105	19	AAH57772	Musca domestica vo
42	3554.5	38.7	2105	20	AAH95777	Calcium permeable
43	3550.5	38.7	2104	19	AAH57773	Musca domestica vo
44	3550.5	38.7	2104	20	AAH95758	Calcium permeable
45	3532	38.5	2100	20	AAH95759	Calcium permeable

ALIGNMENTS

RESULT 1

AAV41668
ID AAV41668 standard; Protein: 1765 AA.
AC AAV41668;
XX
DT 03-DEC-1999 (first entry)
XX
DE Rat sensory neurone specific 2a protein sequence.
XX
KW Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;
voltage gated; hypersensitivity.
XX
OS Rattus sp.
XX
PN WO9947670-A1.
XX
PD 23-SEP-1999.
XX
PF 18-MAR-1999; 99WO-GB00838.
XX
PR 18-MAR-1998; 98GB-0005793.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Grose DT, Hick CA, Tate SN;
XX
DR WPI; 1999-562112/47.
XX
N-PSDB; AAZ21480.
XX
PT Mammalian sodium channel protein for treating pain and hypersensitivity
XX
PS Claim 1; Page 59-64; 73pp; English.
XX

KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
 KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
 KW neuropathic pain; migraine; headache.
 XX Rattus sp.
 XX FR2771103-A1.
 XX 21-MAY-1999.
 XX 19-NOV-1998; 98FR-0014551.
 XX 20-NOV-1997; 97US-0066225.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Dietrich PS, Fish LM, Khare R, Rabert DK, Sangameswaran L;
 XX WPT; 1999-315739/27.
 DR N-PSDB; AAX60241.
 XX Isolated DNA encoding sodium channel of the nervous system
 PT Claim 17; Fig 2A-F; 90pp; French.
 XX
 CC The present sequence represents a type 5 sodium channel protein
 CC designated PN5. The protein is a sodium ion channel of the
 CC nervous system, and is highly expressed in plexiform and dorsal
 CC root ganglia. The protein can be used to identify inhibitors of
 CC sodium channel proteins that are resistant to tetrodotoxin (TTX).
 CC The inhibitors are potentially useful for treating epilepsy,
 CC stroke, diabetic neuropathy, traumatic injuries, AIDS-related
 CC neuropathy, and especially neuropathic pain, e.g. migraine and
 CC headache.
 XX
 SQ Sequence 1765 AA;

Query Match 99.8%; Score 9153; DB 20; Length 1765;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1760; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEERYYPVPEPDERNRPFTSDSLAAIKKRIAIOKERKKSKDAAAEPPQRPQLDLKASR 60
 DB 1 meeryyvpvfpderrnfrpftsdslaiekraiaqkerkkskdkaaepprpqldlksar 60
 QY 61 KLPLKYGDIPELVTKPLEDLDPYKDKHTFMVLNKKRTIYRFSAKRALFTLGPENLRS 120
 DB 61 klpklygdipelvtkpiledldpykdkhtfmvlnkkrtlyrfsakralflgpnflrs 120
 QY 121 LMIRISVHSVSMFIICVTIINCMMANSMERSFDNDIPEYVFIGIVILEAVIKILARGF 180
 DB 121 lmirisvhsvsmfiictvtiincmmansemersfdndipeyfigivileavikilargf 180
 QY 181 IVDFSEFLRDPWNWLDIVGTATATCPGQVNLALRTPRPRALKAKAISVIGLKVIV 240
 DB 181 ivdfseflrdpwnwldivgtatatacpqgvnlalrtprpralkaisvisglkviv 240
 QY 241 GALLRSVKKLVDMVNLTLFCLSIIFALYGOQLFMGILNQCIIKHNCGNPNASNKDCFEKEK 300
 DB 241 gallrsvkkvdmvnltlfclsisifalvgoolfmgilnqcikhnncgnpnasnkdcfekek 300
 QY 301 DSEDFIMCGTWLGRPCPNGSTCDKTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLY 360
 DB 301 dsedfimcgtwlgRPCPNGSTCDKTLNPDNNYTKFDNFGWSFLAMFRVMTQDSWERLY 360
 QY 361 RQILRTSGIVFFVFFVIFIGSPYLLNLTAVVTMAYEONRNVAATEAKEKMFQEAQ 420
 DB 361 rqlirtsgivffvffvifigspyllnltlavvtmayeqnrvaaeteakekmfqeaq 420
 QY 421 QLLREEKALVAMGIDRSSLNLSQASSFSPPKKRFFGSKTRKSFPMGSKTAQASADSE 480
 DB 421 qlireekalvamgidrsslnlsqassfsppkkrrffgsktrksfpmrgsktagasads 480

481 DDASKNPQLLEQTKRLSONLPVDLDEHVDPLHRQRALSAYSILITITIQEKEQPCFP 540
 QY 481 ddasknpqlleqtkrlsonlpvdldehvdplhrqralsaysilittiqeekqpcfp 540
 DB 481 ddasknpqlleqtkrlsonlpvdldehvdplhrqralsaysilittiqeekqpcfp 540
 QY 541 CGKNLASKYLWDCSPQWLCKIKKVLRTIMTDPFTTELAITICIIINTVFLAVEHHMDDNL 600
 DB 541 cgknlaskylwdcspqwlckikvltimtdpfttelaiticiciintvflavehnmddnl 600
 QY 601 KTIILKIGNWVFTGIFIAEMCLIKIILADPYHYFRHGNVDFDSIVALISLADLYNTLSNN 660
 DB 601 ktiilknwvftgifiemclikiiladpyhyfrhgnvdfdsivalisladlyntlsnn 660
 QY 661 RSFLASRLVRFVKLAKSWPTLNTLIKLIHSGVAGLNLTVLTVVVFIFSWGMRFGT 720
 DB 661 rsflasrlvrfvklakswptlntliklihsgvagnltvltvfvfswgmrlfgt 720
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 DB 721 kfnktatqerprrrwhmdnfylvfvfrilcgewienmgcmqmdgspclivfl 780
 QY 781 IMVIGKLVNLFTALLNLSFSENEEKDGLSEGETRKTQVOLALDRFRRAFSLMHALQSF 840
 DB 781 imvigklvnlftallnlsfseekdglsetrktkvqaldrfrfafslmhalqsf 840
 QY 841 CCKCRKRNPKPKETTESFAGENKDSITLPDARPWKEYDTDMALYTGOAGAPLAEVE 900
 DB 841 cckcrrknspkpkettesfagenkdsitlpdarpwkeydtmalytgoagaplaeve 900
 QY 901 DDVEYCEGEGALPTSHSAGVQAGDLPPETKQLTSPDDQGVMEVFSEEDLHLSIQSPRK 960
 DB 901 ddveycyeggalptshsagvqagdlpetkqltspddqgvemevfseeditlhlisqsprk 960
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 QY 1021 WNIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPQVEKLLRCRDNFTFTFL 1080
 DB 1021 wnirktcyqivkhswfesfiifvillssgalifedvnlpsrpqvekkllrcrdnftftfl 1080
 QY 1081 LEMILKWVAFGRFYFTSANCWDLFLIVVSVLSLNNLPSLKSFTLRALRPLRALSQFE 1140
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 QY 1141 GMKVVVVALISAIPAILNVLVCLIFWLVFCLGNLPSFGKFGRCINGTDINMYLDFTEV 1200
 DB 1141 gmkvvvvalisaipailnvlvclifwlvfclgnlpsfgkfgrcingtdinmyldftev 1200
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 QY 1261 NLYAYLVFVFIIFGSEFTLMLFGIVIDNFNOQKKLGGQDIFWTEBQKYYNAMKKLG 1320
 DB 1261 nlyaylvfvfiifgsftlmlfgiuidnfnoqkklggqdifwtebqkyynamkklg 1320
 QY 1321 TKKPKQPIPRPLNKOAFVFDLVTSOVFDVILGLIVLNMIMMAESADQPKVKYTFDI 1380
 DB 1321 tkkpkpiproplnkofvfdlvtsovfdvilglivlnmimmaesadqpkvktfdi 1380
 QY 1381 LNIAPVFIITIECLIKVPALRQHYFTNGWNLFDVCVVVVLSTIISTLVSRLESDISFPPTL 1440
 DB 1381 lniapvfiitieclikvfallrqhyftngwnlfdcvvvvlsistlvsrledsdisfpptl 1440
 QY 1441 FRVRLARIGRILRLVRAARGIRTLLEFALMMSLSFLNIGLILLFLVMPITYAIFGMSWFSK 1500
 DB 1441 frvrlarigrilrlvraargirtllfalmslpslfnigllflvmpityaifgmswfsk 1500
 QY 1501 VKKSGIDDIINFETFTGSMCLCLFIQITTSAGWDTLNPNMLEAKEHCNCSODSCQOPIA 1560
 DB 1501 vkksgiddiinfetftgsmclclfiqittsagwdtlnpmlakehcnscsodscqqpia 1560

Qy 1561 VVYFVSXIIISFLIVNMVYIAVILENNTATESEDPAGEDDFEIFYEYWEKFDPEASQF 1620
Db 1561 VVYFVSXIIISFLIVNMVYIAVILENNTATESEDPAGEDDFEIFYEYWEKFDPEASQF 1620
Qy 1621 IQYSALSDFDALPEPLRVAKPNKQFLVMDLPMVMGDRHLHCDVLFATFTRVLGDSSGL 1680
Db 1621 IQYSALSDFDALPEPLRVAKPNKQFLVMDLPMVMGDRHLHCDVLFATFTRVLGDSSGL 1680
Qy 1681 DTMKTMEEKFMEANPKKLYEPIVTTTKRKEEBOGAIVQRAYRKHMVKMLRLKDRS 1740
Db 1681 dtmktmeekfmeanpfkkyepivtttkrkeeeqgaaviqrayrkhmekmvklrlkdrs 1740
Qy 1741 SSSHQVFCNGDLSSLDVAKVKVHND 1765
Db 1741 ssshqvcngdsslslvdkvkvhnd 1765
RESULT 3
AAY06596 ID AAY06596 standard; Protein; 1765 AA.
XX AC AAY06596;
XX DT 26-OCT-1999 (first entry)
XX DE Rat sodium channel NaN.
KW NaN; sodium channel; ion transport; rat; dorsal root ganglia;
KW pain; paraesthesia; hyperexcitability; therapy.
XX OS Rattus sp.
XX PH Key
FT Region 125..148 Location/Qualifiers
FT /label= DI-S1
FT /note= "domain I transmembrane segment S1"
FT Region 157..177
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FT Region 191..210
FT /label= DI-S3
FT /note= "domain I transmembrane segment S3"
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FT /label= DI-S4
FT /note= "domain I transmembrane segment S4"
FT Region 254..273
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XX WO938889-A2.
PN Ser-355 residue is implicated in the TTX-R phenotype"
XX 05-AUG-1999.
XX 29-JAN-1999; 99WO-US02008.
XX 20-NOV-1998; 98US-0109402.
XX 29-JAN-1998; 98US-0072990.
XX (UYA) UNIV YALE.
XX Dlb-Hajj S, Waxman S;
XX WPI; 1999-479168/40.
XX N-PSDB; AAX87600.
XX New isolated nucleic acids encoding sodium channels, used to develop
XX products for treating acute or chronic pain or hyperexcitability
XX phenomena

PS Claim 1; Fig 2A-C; 91pp; English.

This is the predicted amino acid sequence of the rat NaN channel, as deduced from isolated rat NaN cDNA (see AAX87600). NaN is a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a ^{90}Sr -R sodium current. Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord.

AA	Sequence	1765 AA;
SQ		

Query Match	99.78;	Score 9149;	DB 20;	Length 1765;
Best Local Similarity	99.78;	Pred. No. 0;		
Matches 1759;	Conservative 4;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	MEERYYPVIRPDERNFRPPTSDSLAAIKKRTAIOKERRKSKDKAAAEQPPRPOLDLKASR	60	
Db	1	meeryypvirdernfrpptsdsllaaikkrtaiokerkksdkdaaaepqrpoldlksr	60	
Qy	61	KLPLKYGDPPELVTKPLEDDPYVYKHKTFMWJNKKRTIYRFSAKRALFILGPPNPURS	120	
Db	61	kplklygdppelvtkpleddpyvykhtfwmjnkkrtyrfsakralfilgppnpurs	120	
Qy	121	LMIRISVHVSFMFICTVIINCMPMANSERSFNDIPYVFGIYILEAVIKILARGF	180	
Db	121	lmirisvhsfsmfiictviincmfmansersfndipyvfygilyleavikilargf	180	
Qy	181	IVDEFSFLURDPWNWLDFTVIGTATATCPGSGOVNLSALTRFVRFRALKAVISISGLKTV	240	
Db	181	ivdefslrdpwnwldftvigtatatcpfsgsqvnlsalrtfrvfralkavisisglkv	240	
Qy	241	GALLRSVKKLVDVMVLTLCISIFALVGOQLFMGILNOKICKHNCGPNPASNKDCFEKEK	300	
Db	241	gallrsvkklvdvmvltlfcisifalvgqqlfmgilnokickhncgpnpsnkdcekek	300	
Qy	301	DSEDFIMCGTWLGRPCPNGSTCKDTTLNPDDNNTYTKFDNFGNSFLAMFRVMTQDSWERLY	360	
Db	301	dsedfimcgtwlgrrpcpnsgstckdtlnpdnnnytkfdngswflamfrvmtqdswe	360	
Qy	361	ROIILRTGIYFVFFVFWVIFIGSGFVLLNLTAVTMMAYEEQNRRNVAATEAKEKMFQEAQ	420	
Db	361	rqiilrtagiylvffvfwvifigsfyllnltlavtmmayeegnrvaaeteakekmfqa	420	
Qy	421	QLLREEKALVAMGIDRRSLNSLQASSPSPKRRKFFGSKTRKSPFMRGSKTAQASADSE	480	
Db	421	qlleekaalvamgidrrslnsllqasspspkrrkffgsktrksfmrgrsktaqasads	480	
Qy	481	DDASKNPOLLEQTKRLSONLPVDLFDEHVDPLHQRALSAVSILTTITQEBKFPQPCFP	540	
Db	481	ddasknpqlleqtkrlsqnlpvdlfdehvdplhqralsavsiltitmqeqekfdepcfp	540	
Qy	541	CGKNLASKYLVWDCSPOWLCTIKKVLRTIMTPDPFEFLATICTIINTVFLAVEHHNDDNL	600	
Db	541	cgknlaskylvwdcspowlctikkvlrtimtdpffeelatictiintvflavehnmddnl	600	
Qy	601	KTILKIGNWVFTGIFIAEMCKLIIALDPYHYFRHGWNVFDSITVALLSLADLYNTLSNN	660	
Db	601	ktilkignwvftgiaemckliialdpdpyhyfrhgwvnvfdsisallsladlyntlsdn	660	
Qy	661	RSFTLASRLVRFVFKLAKSWPTNLTLIKTIHGSVGALGNLTVTLTVTFVFSVGMRLFGT	720	
Db	661	rslfslasrlvrfvfklskswptnltlkighsvgalgnltvltvtfvfvsvgmrlfgt	720	

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RESULT      4
AAB20122
ID   AAB20122 standard; Protein; 1765 AA.
XX
AC   AAB20122;
XX
XX 30-APR-2001 (first entry)
XX
XX Rat sodium channel NaV.
XX
XX Sodium channel; NaV; rat; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
KW diagnosis.
XX
XX
XX Key Location/Qualifiers
FT Domain 125..148
FT /note= "transmembrane domain DI-S1"
FT Domain 157..177
FT /note= "transmembrane domain DI-S2"
FT Domain 191..210
FT /note= "transmembrane domain DI-S3"
FT Domain 216..237
FT /note= "transmembrane domain DI-S4"
FT Domain 254..273
FT /note= "transmembrane domain DI-S5"
FT Domain 338..350
FT /note= "transmembrane domain DI-S5"
FT Domain 353..358
FT /note= "transmembrane domain DI-S5"
FT /note= "transmembrane domain DI-S5", includes Ser
FT residue at position 355 implicated in
FT tetrodotoxin resistance"
FT
FT Domain 371..398
FT /note= "transmembrane domain DI-S3"
FT Domain 567..591
FT /note= "transmembrane domain DII-S1"
FT Domain 603..624
FT /note= "transmembrane domain DII-S2"
FT Domain 633..654
FT /note= "transmembrane domain DII-S3"
FT Domain 663..682
FT /note= "transmembrane domain DII-S4"
FT Domain 699..719
FT /note= "transmembrane domain DII-S5"
FT Domain 741..750
FT /note= "transmembrane domain DII-SS1"
FT Domain 755..759
FT /note= "transmembrane domain DII-SS2"
FT Domain 774..800
FT /note= "transmembrane domain DII-S6"
FT Domain 1029..1052
FT /note= "transmembrane domain DII-S1"
FT Domain 1067..1192
FT /note= "transmembrane domain DIII-S2"
FT Domain 1198..1116
FT /note= "transmembrane domain DIII-S3"
FT Domain 1119..1140
FT /note= "transmembrane domain DIII-S4"
FT Domain 1159..1180
FT /note= "transmembrane domain DIII-S5"
FT Domain 1223..1232
FT /note= "transmembrane domain DIII-SS1"
FT Domain 1236..1241
FT /note= "transmembrane domain DIII-SS1"
FT Domain 1263..1288
FT /note= "transmembrane domain DIII-S6"
FT Domain 1341..1356
FT /note= "transmembrane domain DIV-S1"
FT Domain 1440..1463
FT /note= "transmembrane domain DIV-S4"
FT Domain 1479..1501
FT /note= "transmembrane domain DIV-S5"
FT 1513..1527

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FT /note= "transmembrane domain DIV-SS1"
FT 1529..1534
FT /note= "transmembrane domain DIV-SS2"
FT 1558..1584
FT /note= "transmembrane domain DIV-S6"
XX
XX Rattus norvegicus.
OS
XX WO200105831-A1.
PN
XX 25-JAN-2001.
PD
XX 14-JUL-2000; 2000WO-USI9342.
FF
XX 16-JUL-1999; 99US-0354147.
PR
XX (UYYA ) UNIV YALE.
PA
XX Dib-Hajj S, Waxman SG;
PI
XX WPI: 2001-103147/11.
UR
XX N-PSDB; AAF30102.
DR
XX
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium
PT channels, useful for preventing, diagnosing and treating pain,
PT paraesthesia and/or hyperexcitability phenomena -
PT
XX Example 2; Fig 3; 162pp; English.
PS
XX
XX The present sequence is that of novel rat tetrodotoxin resistant
CC sodium channel NaV, as deduced from cDNA (see AAF30102) isolated
CC from a rat dorsal root ganglia tissue library. The sequence
CC shows 69% similarity to human NaV (see AAB20121). NaV belongs to
CC the a-subunit voltage-gated sodium channel protein family. It
CC produces a TTX-R sodium current. Such channels underlie the
CC generation and propagation of impulses in excitable cells such as
CC neurons and muscle fibres. Preferential expression of NaV on
CC sensory neurons innervating the body (dorsal root ganglia) and
CC the face (trigeminal ganglia), but not on other neurons, makes
CC it a very useful target for diagnostic and/or therapeutic uses in
CC relation to acute and/or chronic pain pathologies. A claimed
CC method of treating pain, paraesthesia and/or hyperexcitability
CC phenomena in a human or animal subject involves administering an
CC agent that alters sodium current flow through NaV channels, or
CC which modulates transcription or translation of NaV mRNA, in
CC dorsal root ganglia or trigeminal neurons. NaV polypeptides can
CC be obtained by recombinant expression, and used to treat disorders
CC associated with decreased sodium channel expression, to screen for
CC compounds that modulate sodium channel expression or activity,
CC and to raise antibodies useful as diagnostic agents.
XX
XX Sequence 1765 AA;
SQ

```

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Query Match 99.7%; Score 9149; DB 22; Length 1765;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1759; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEERYYPVIFPDENFRPFTSDSLAAIKKRIATQKERRKSKDAAEPPQRPQLDKASR 60
Lb 1 meeryypvifpdernfrpftsdslaiekriaiekrrkkskdaaepprpqldlksar 60
Qy 61 KLPKLYGDIPELVTKPLEDLDPPYKDKHTFMVNLKRRTIYRFSAKRALFILGPNPLRS 120
Lb 61 klpklygdippelvtkpleldldppykdkhtfmvlnkrrtiyrfsakralfilgpnplrs 120
Qy 121 LMIRISVHSVFSMFIICTVIINCMFMANSMERSFDNDIPEYVFIQIVILEAVIKLARGF 180
Lb 121 lmirisvhsvfsmfiictviincmfmanmsmersfdndipeyvfiiyleavikilargf 180
Qy 181 IVDEFSFLRDPWNWLDIFIVIGTAITATCPGQVNLASALRTRFVRFAKKAISVISGLKVIV 240
Lb 181 ivdefslrldpwnwldfivigtaitatcpgsqvnlsalrtfrvfralkaisvisglkviv 240

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QY 241 GALLRSYKVLVDVWMLTFLCLISFALVGOQLFMGILNOKICKHNCGPNPASNKDCFEKEK 300
DB 241 gallrsykvkvlvdvwmvltlclisfalsalvgqqlfmgilnqkckhncgpnasnkdcfekek 300
QY 301 DSEDFMCGTWLGRPCPNSTCDKTTPLNDNNYTKFDNFGWSFLAMFRVMTQDSWERLY 360
DB 301 dsedfmcgwtwlgprcpcnstcdkttplndnnytkfdnfgwsflamfrvmtqdswerly 360
QY 361 RQILRTSGIYVFVFVFFVIFLGSFYLENLTLAVVTMAYEQNRNVAATEAKEKMFQEAQ 420
DB 361 rqiirtsgiyvfvffvffviflgsfylnltlavvtmayeqnrnvaaeteakekmfgeaq 420
QY 421 QLREEKEALVAMGIDRSSUNLSQASSFSPPKRRKFFSGTKRKSFFMRGSKTAQASADSE 480
DB 421 qlireekealvamgidrssunlsqassfsppkrrkffsgtkrksffmrsgsktaqasadse 480
QY 481 DDASKNPOLLKQNLSONLPVDLFDEHVDPLHRQALSAVSILTIITIOGEKEFQECFP 540
DB 481 ddasknpqlleqtkrlsqnlpvdlfdehvdplhrqalsavsilittioqekefgecpfp 540
QY 541 CGKNLASKYLWDCSPQWLCKIKKVLRTIMTDPFTELAITICIIINTVFLAVEHNMDDNL 600
DB 541 cgnkaskylwdcspqwlckikvrlrtimtdpftelaiticiiintvflavehnmddnl 600
QY 601 KTLKIGNWVFTGIFIAEMCLKIIFALDPYHYFRHGWNVFDSIVALSLADLYNLSDNN 660
DB 601 ktlkignwvftgifiuemclkiialdpqpyhyfrhgwvnvfdsaivalsladlynltsdnn 660
QY 661 RSFLASRLVRFKLAKSWPTLNTLKIIGHSVGALGNLFWLTVIVFISVWGMRLFGT 720
DB 661 rsflasrlrvrfklakswptlntlkiighsvgalgnltvltvltvifsvvgmrlfgt 720
QY 721 KFNKTAYATQPRRRHMDNYHSFLVVPRIICGWIENWGMQMDGSPLCIIVFVL 780
DB 721 kfnktayatqprrrhmdnyfhsflvvpriicgewienwgmqmdgspclciivfl 780
QY 781 IMVIGKLVNLFIALLNSFSNEEKDGLSEGETRKTQVQALDRFRRAFSPFMLHALQSF 840
DB 781 imvigklvnlfiallnfsneekdglsegetrktkvqaldrfratfsmhalqsf 840
QY 841 CCKKCRKNSPKPKETTESFAGENKDSILDPARPKWEYDTDMALYTGQAGAPLAPAEVE 900
DB 841 cckkcrknsppkpkettesfagenkdsilpdrpkweydtmalytgagaplapaeve 900
QY 901 DDVEYCGEGGALPTSHSAGVQAGDLPPETKQLTSPDDQGVMEVFSEEDLHLSIQSPRK 960
DB 901 ddveycgeggaltshsagvqagdlppetkqltspddqgvmevfseedlhlsiqsprk 960
QY 961 KSDAVSMLSECTIDLNDIFRNLOKTVSPKKQDPCFPKGLSCHFLCHKTDKRSPPWVLW 1020
DB 961 ksdavsmsectidlndifrnloktvspkkqdpccfpkglischflchktdkrspwvlw 1020
QY 1021 WNIKRTQYIKVHSWFSFIFIVILLSSGALIFEDVNLPSRPQVEKLLRCRTDNTFTIFL 1080
DB 1021 wnirktyqyikvhsfswfsfifivillssgalifedvnlpsrpqveklrcrtdnftifl 1080
QY 1081 LEMILKVVAGCFRBYFTSANCWLDLIVVYVSLMNLPSLKSFRTLRALPLALSOFE 1140
DB 1081 lemilkvvagcfryftsancwldlilvvysvlmnlpslksfrtlralplalsqfe 1140
QY 1141 GMKVYVALISAIPAILNLVLLVCLIFWLVCILGNLVPFSGKFGRCINGTDINMYLDTEV 1200
DB 1141 gmkvvyvalisaipailnlvllvclifwlvclgnlvfsgkfgrcingtdinmyldtev 1200
QY 1201 PNRSQCNISNYSWKVPQVFNQVNGVAYLALQVATYKGLWEIMNAAVDSREKDPDFEA 1260
DB 1201 pnrscqcnisnyswkvpqvnqvnaylallqvatykgwleimnaavdsrekdpdfea 1260
QY 1261 NLXAYLFFVVFIFPGSFFTLNLFTGVIIIDNPNQOQKLGODIPMTBEQKYYNAMKKLG 1320
DB 1261 nlxaylffvfvfifpgsftlnlftgviiidnfnqgqkkggdiifmteeqkyynamkklg 1320

RESULT 5

AAB20123
ID AAB20123 standard; Protein; 1765 AA.
XX
AC AAB20123;
XX
DT 30-APR-2001 (first entry)
XX
DE Rat sodium channel NaN.
XX
KW Sodium channel; NaN; rat; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
XX diagnosis.
FH Key Location/Qualifiers
FT Domain 125..148
FT FT /note= "transmembrane domain DI-S1"
FT Domain 157..177
FT FT /note= "transmembrane domain DI-S2"
FT Domain 191..210
FT FT /note= "transmembrane domain DI-S3"
FT Domain 216..237
FT FT /note= "transmembrane domain DI-S4"
FT Domain 254..273
FT FT /note= "transmembrane domain DI-S5"
FT Domain 338..350
FT FT /note= "transmembrane domain DI-Ss1"
FT Domain 353..358
FT FT /note= "transmembrane domain DI-Ss2, includes Ser
residue at position 355 implicated in
tetrodotoxin resistance"
FT Domain 371..398
FT FT /note= "transmembrane domain DI-Ss3"
FT Domain 567..591
FT FT /note= "transmembrane domain DII-S1"
FT Domain 603..624
FT FT /note= "transmembrane domain DII-S2"
FT Domain 633..654
FT FT /note= "transmembrane domain DII-S3"
FT Domain 663..682

FT			/note= "transmembrane domain DII-S4"
FT	Domain	699..719	
FT	Domain	/note= "transmembrane domain DII-S5"	
FT	Domain	741..750	
FT	Domain	/note= "transmembrane domain DII-SS1"	
FT	Domain	755..759	
FT	Domain	/note= "transmembrane domain DII-SS2"	
FT	Domain	774..800	
FT	Domain	/note= "transmembrane domain DII-S6"	
FT	Domain	1029..1052	
FT	Domain	/note= "transmembrane domain DIII-S1"	
FT	Domain	1067..1192	
FT	Domain	/note= "transmembrane domain DIII-S2"	
FT	Domain	1198..1116	
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FT	Domain	/note= "transmembrane domain DIII-S5"	
FT	Domain	1223..1232	
FT	Domain	/note= "transmembrane domain DIII-SS1"	
FT	Domain	1236..1241	
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FT	Domain	1263..1288	
FT	Domain	/note= "transmembrane domain DIII-S6"	
FT	Domain	1341..1356	
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FT	Domain	/note= "transmembrane domain DIV-S5"	
FT	Domain	1513..1527	
FT	Domain	/note= "transmembrane domain DIV-SS1"	
FT	Domain	1529..1534	
FT	Domain	/note= "transmembrane domain DIV-SS2"	
FT	Domain	1558..1584	
FT	Domain	/note= "transmembrane domain DIV-S6"	
FT	Misc-difference	652	
FT		/note= "encoded by CTN"	
FT	Misc-difference	1334	
FT		/note= "encoded by AAN"	

AA
OS
Rattus norvegicus.

AA
PN
WO200105831-A1.

25-JAN-2001.

XX
PF 14-JUL-2000; 2000WO-US19342.

16-JUL-1999; 99US-0354147.

XX PA (UYYA) UNIV YALE.

XX
PI Dib-Hatt S. Waxman SG:

WPI: 2001-103147/11.

DR WFL, 2001 105147/1
DR N-PSDB; AAF30102.

Nucleic acid molecules encoding human tetradotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -

Example 2; page 98-103; 162pp; English.

The present sequence is that of novel rat tetrodotoxin resistant sodium channel NaN, as deduced from cDNA (see AAF30102) isolated from a rat dorsal root ganglia tissue library. The sequence shows 69% similarity to human NaN (see AAB20121). NaN belongs to the α -subunit voltage-gated sodium channel protein family. It produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on

sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through Na⁺ channels, or which modulates transcription or translation of Na⁺ mRNA, in dorsal root ganglia or trigeminal neurons. Na⁺ polypeptides can be obtained by recombinant expression, and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate sodium channel expression or activity, and to raise antibodies useful as diagnostic agents.

Sequence 1765 AA;

Query Match	99.7%	Score 9141;	DB 22;	Length 1765;
Best Local Similarity	99.6%	Pred. No. 0;		
Matches 1758; Conservative		3; Mismatches	4; Indels	0; Gaps

Qy	1	MEERYPVTFPPDERNRPFTTSSLAALKKRIATOKERKKSOKKAAAEPPQRPOLDLKASR	60
Db	1	meerypvtfppdernrpfTsdslaalekriaIqkerkkskkaaepprpqldlkasr	60
Qy	61	KLPKLXGDIPELVTKPLEDLPYVKDHTFMVLNKKRTIYRSAKRALFILGPNPLAS	120
Db	61	kIpklygdipelpvTkpleDlpYvkDhtfMvlnKkrtIyrsakRaLfiLgpnPlas	120
Qy	121	LMIRISVHSVSMFICTVIINCWMANSMERSFDMIDPEYVIGIYVILEAVIKILARGF	180
Db	121	lMirisvhsvsmfiCtviInCwmansmersfDmIdpeyViGiYvileavIKilargf	180
Qy	181	IVDEFSFLRDPWNWLDPEVITGTAIATCFPGSQVNLGSALRTFRVFRALKAISVISGUKVIV	240
Db	181	ivdeFsflrDpwnwldpeViTgtaIatCfpgsqvnlGsAlrtFrVfrAlkaiSvisgUkviV	240
Qy	241	GALLRSVKKLVDMVWVLTFLCFLSFALVGOQLPFGILNOKICKHNCCPNPASNKDCFEKEK	300
Db	241	gallrsVkkLvdmVwVlTfLcflSfAlvGoQLpfgILnOkIckHnccpnPasnKdcFekeK	300
Qy	301	DSEDFIMCGTWLGRPCPNGSTCDKTTLPNDNNYTKFDNFGWSFLAMFRVMTODSWERLY	360
Db	301	dseDfImcgtwlgRpcpnGstcdKtTLpndNnytkfDnfgwsflamFrVmtodSwerly	360
Qy	361	RQILRSGIYVFVFVVVIFLGSFYLLNLTLAVVTMAYEBOQNRNVAEATEKMKMQEQAQ	420
Db	361	rQilrtsgiyVfvfVvVvIfLgSfyLLnLTlAvVtmAYeBoQnrNvAEateKmkmqeQaQ	420
Qy	421	QLLREKEALVANGIDRSSLNSLQASSFSPKPKRFFGSKTRKSFPMRGSKTAQASADSE	480
Db	421	qllReeKealvAngIdrSSlNsLqassfSpkRkRffgSkTrkSfPMrgSkTaqasadse	480
Qy	481	DDASKNPQLLEQTKRISQNLVPDLDEHVDPLHRQALSAVSILTITIOEQERFQBPCCFP	540
Db	481	dDasknpqlleqtkRisqnlVpdlDehvdPlhrqalSavsiltitIOeqerfQbpccfp	540
Qy	541	CGKNLASKYLVWDCSQOWLICIKKVLRTIMTDPTELAITICIINIIVFLAVEHHNNDDNL	600
Db	541	cGknLaskyLvwdcSqowliCikKvlrtImtdpTeLaIticiIiniVflaveHhnnDnl	600
Qy	601	KTILKTGNWVFTGFIETACMLKTIIALDPYHYPRHGNVFDISIVALLSLADLVNTLSDDNN	660
Db	601	kTilKtgnwVftGfietaCmLkTiIalDpyHyprHgnvfdiSiVallsladLVntlsDnn	660
Qy	661	RSELASLRLVRFKLAKSWPTNLTKIIGHSGVGLGNLTVTLTVIVFVFSVVGMRLFGT	720
Db	661	rSelaSlrLvrFklakSwptnlTkiIGHsvglGNltVtlTVIvFvFSvvgmrLfgT	720
Qy	721	KFNKTAYATQERPRRRHHMDNFVHSELVFRILCGEWIENWGCMDMGSPLCIIVFVL	780
Db	721	kfnkTayateqerprrrhHmdnfVhseLvfrilCGewienwgcmdmgspLciivfvl	780

Qy 781 IMVIGKLVNLFIALLLNSFSNEEKDGLSEGETRKTQVQALDRFRRAFSFMLHALQSF 840
Db 781 Imvigklvlnlfialllnsfsneekdgslegetrktkvqaldrfrfrafsmhalqsf 840
Qy 841 CCKCRKRNKPKETTESPAGENKDSLTPARPKWKEYDTDMALYTGAGAPLAPAEVE 900
Db 841 cckckrrnspkpkettespagenkdsllparpwkeytdtmdalytgagaplapaeve 900
Qy 901 DDVEYCEGGALPTSOHSAGVQAGDLPETKQLTSPDDQGVEMEVFSEEDLHLSIQSPRK 960
Db 901 ddveyceggalptsohsagvqagdlppetkqltspddqgvemevfseedhlhlsiqsprk 960
Qy 961 KSDAVSMLSEGSTIDLNDIFRNALQTVSPKQPDRCFPKGLSCHFLCHTKDKRKSPWYLV 1020
Db 961 ksdavsmllsegstidlndifrnalqtvspkqpdrccfpkglkschflchtkdkrkspwylv 1020
Qy 1021 WNIKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLPSRPOVEKLLRCDNIFTFIFL 1080
Db 1021 wnirktcyqivkhswfesfiifvillssgalifedvnlpsrpovekllrctdniftfifl 1080
Qy 1081 LEMILKWVAFGRFRYFTSAWCWDLFIIVVSVLSLMLNPLSKSPRTLALPLRLALSQFE 1140
Db 1081 lemilkwvafgrfryftsawcwlfdliivvsvlsmlnplsksftrtlalplrlalsqfe 1140
Qy 1141 GMKVYVVALISAIPAILNLVLCILFWLVLFCILGVNLFSGRGCINGTDINMYLDFTEV 1200
Db 1141 gmkvvyvalisaipailnlvllcflwlvfclgvnlfsgrgfcngtdinmyldftev 1200
Qy 1201 PNRSCNLSNYSWKVPQVNFNNGVAYLALQVATYKGLWEIMNAVDSRDKSQPDPEA 1260
Db 1201 pnrsqcnlsnyswkvpqvnfnvngaylallqvatykgwleimnaavdsrdekdpdea 1260
Qy 1261 NLXAYLVFVPTIFGSPFTLLFTGVITDNEQOQKLGIGDIFWTEQKYYNAMKKLG 1320
Db 1261 nlxyaylvfvtifgspftllftgvitdneqoqkllgigdiwteqkyynamkklg 1320
Qy 1321 TKKQKPIPRNLKQAFVDFVLTSQVFDVIIIGLVLNMIIMMAESADQPKDKVKTPTDI 1380
Db 1321 tkkqkpiprnlkxqafvdlvtsqvfdiilglvlnmiimmaesadqpkdkvktptdi 1380
Qy 1381 LNIAPVIFTTECLIKVPALQHFVTNGWNLFDVWVVLSTIISLVSLESDISFPPTL 1440
Db 1381 lniapviftteclikvpalkhfvtngwnlfdcvvvvlsistlvslrledsdisfpptl 1440
Qy 1441 FRVRLARIGRILRLVRAARGIRTLFALMMSLPSLFGNIGLLFLVMPFIYAFGMSWFSK 1500
Db 1441 frvrlarigrilrlvraargirtllfalmslpslfnigllflvmpfiyafgmswfsk 1500
Qy 1501 VKSGGIDDIFFNETFTGSMCLFQITTSAGWDTLLNPMLEAKHCNSSQDSQQQOIA 1560
Db 1501 vksggiddifnetftgsmclfqittsagwdtllnplmleakehcnssqdsccqoia 1560
Qy 1561 VYFVSYIIISFLIVNMYIAVILENFNTATESEDPIGEDDFEIFYEVWEKFDPEASQF 1620
Db 1561 vyfvsyiiiisflivnmymyiavilenfnntateesedpiledgfeyevwekfdepeasqf 1620
Qy 1621 IQYSALSDFADALPEPLRVAKPNKFOFLVMDLPMVMGDRLCMDVLFATFTRVLGDSGL 1680
Db 1621 iqysalsdfadalpeplrvakpnkfqlvmdlpmvmgdrhcmdivlftftrvlgdssgl 1680
Qy 1681 DTMKTMEEKPMEANPKKLEPIVITTTKRKEEQGAAGVIRAYRKHMEKMKVRLKDRS 1740
Db 1681 dtmktmEEKPMEANPKKLEPIVITTTKRKEEQGAAGVIRAYRKHMEKMKVRLKDRS 1740
Qy 1741 SSSHQVFCNGDLSLDVAKVKVHND 1765
Db 1741 ssshqvfcngdlsldvakvkvhnd 1765
RESULT 6
AA06597
ID AA06597 standard; Protein; 1765 AA.
XX

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W09938889-A2.

05-AUG-1999.

29-JAN-1999; 99WO-US02008.

20-NOV-1998; 98US-0109402.

29-JAN-1998; 98US-0072990.

(UYUA) UNIV YALE.

Dib-Hajj S, Waxman S;

WPI; 1999-479168/40.
 N-PSDB; AAX87601.

New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability phenomena

Claim 1; Fig 7B1-2; 91pp; English.

This is the predicted amino acid sequence of the mouse Na^v channel, as deduced from isolated mouse Na^v cDNA (see AAX87601). Na^v is a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. Rat, mouse and human Na^v nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express Na^v, methods for identifying agents that modulate Na^v channel activity or Na^v channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, anaesthesia and hyperexcitability phenomena. The preferential expression of Na^v in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord.

XX Sequence 1765 AA;
 SQ
 Query Match 88.9%; Score 8153; DB 20; Length 1765;
 Best Local Similarity 88.7%; Pred. No. 0;
 Matches 1569; Conservative 94; Mismatches 99; Indels 6; Gaps 5;
 QY 1 MEERYYPVIEPDERFRFTSDSLAAIKKRIATIAOKERKSKDKAAAEPPQPPOLDLKASR 60
 DB 1 meeryypviefderfrftsdslaaikkrtaiaokerkkdkaaatepprpqldlkasr 60
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 DB 61 klplklygdipelvtkpleldppykdkhtpmvlnkkrtiyrfsakralfilgpnplrs 120
 QY 61 klplygdvdpdliakpleldipfydkhtfmvlnkkrtiyrfsakralfilgpnplrs 120
 DB 61 klplygdvdpdliakpleldipfydkhtfmvlnkkrtiyrfsakralfilgpnplrs 120
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 DB 121 lmirisvhsvfmfiictviincmfmanssvdrpsnipeyvfgyileavikilar 180
 QY 179 GFIVDESFELRDPNNWLDIFVIGTAIATCPGSOV--NLSALRTFRVPRAKIAISVSLK 237
 DB 181 gfiwdesfelfrdpnnwldifvigtaiatcpgsqv--nlsalrtfrvpralkaisvisgk 240
 QY 238 VIVGALLRSVKKLVDVMVLTFLCLSIIFALVGOQLFMGILNOKCIKHNGPNPASKDCFE 297
 DB 241 vivgallrsvkkldvdmvltflclsisifalvgqqlfmgilskcikkddcgnafnkdcfv 300
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 DB 301 kendsedfimcgnwlgrrscpdgstcnkttfnpdynntfnsfgwsflamfrvmtqdswe 360
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 DB 361 klyrqrlrtsgiyfvvffvvfvlgsfyllnltavvtmayeqnrvaaatekakekmfq 420
 QY 418 EAQOLLREEKEALVAMGIDRSSLSLOASSPSPKRRFFGSKTRKSPMRGSKTAOASAS 477
 DB 421 eaqollreekealvamgidrtslnslqassfspkrrffgsktrksfmrskktarasa 480
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 DB 481 dseddasknpqlleqtkrlsqnlplvdehvdplhqralsavsiltitmeqekseqep 540
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 DB 541 cfpcknlaskylwecspwlcikvltqtdpftelaiticliintvflamehnmnd 600
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 DB 601 dnlktilkignwvftgifaemckliialdpvhyfrhgnvfnfslvalsladlvfhkls 660
 QY 658 DNNRSLASRLRVLFVKLAKSWPTLNTLIKIGHSVGALNLTVLTITVIFSVVGMRL 717
 DB 661 -knlslasrlrvlrvfklakswptlntlikighsvgalnltvltitvifsvvgmrl 719
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 DB 720 fgatfentkayataqerprrrhmdnpyfslvfrilcewiennmgcmqmdgsgplciiv 778
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Db 1199 snvpnqgcqvsnvtykvnpvndvgnaylallqvetykgwidmnaavdsrgkdeqpa 1258
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Db 1678 sgldtmtmeerfmeanpkklyepivtttkreeeqgaavayqrayrkhmekmkvlrk 1737
QY 1738 DRSSSHQVFCNGDLSSLDVAKVKVHND 1765
Db 1738 grssslqvfcngdlsldvapkikhvd 1765

RESULT 7
AAB20124
ID AAB20124 standard; Protein; 1765 AA.
XX
AC AAB20124;
XX
DT 30-APR-2001 (first entry)
XX
DE Mouse sodium channel Nan.
XX
KW Sodium channel; NaN; rat; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
KW diagnosis.
XX
FH Key Location/Qualifiers
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/note= "transmembrane domain DI-S4"
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/note= "transmembrane domain DIV-S6"

Mus musculus.
WO200105831-A1.
25-JAN-2001.
14-JUL-2000; 2000WO-US19342.
16-JUL-1999; 99US-0354147.
```

PA (UYAA) UNIV YALE.
 XX D1b-Hajj S, Waxman SG;
 XX WPI; 2001-103147/11.
 DR N-PSDB; AAF30103.
 XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium
 PT channels, useful for preventing, diagnosing and treating pain,
 PT paraesthesia and/or hyperexcitability phenomena -
 XX Example 3; Fig 7B; 162pp; English.
 XX
 CC The present sequence is that of novel mouse tetrodotoxin resistant
 CC sodium channel Na_v, as deduced from the Scn1a gene (see AAF30103)
 CC isolated from a mouse trigeminal ganglia cDNA. The sequence shows
 CC 68% similarity to human Na_v (see AAB20121). Na_v belongs to the
 CC a-subunit voltage-gated sodium channel protein family. It produces
 CC a TTX-R sodium current. Such channels underlie the generation and
 CC propagation of impulses in excitable cells such as neurons and
 CC muscle fibres. Preferential expression of Na_v on sensory neurons
 CC innervating the body (dorsal root ganglia) and the face (trigeminal
 CC ganglia), but not on other neurons, makes it a very useful target
 CC for diagnostic and/or therapeutic uses in relation to acute and/or
 CC chronic pain pathologies. A claimed method of treating pain,
 CC paraesthesia and/or hyperexcitability phenomena in a human or
 CC animal subject involves administering an agent that alters sodium
 CC current flow through Na_v channels, or which modulates transcription
 CC or translation of Na_v mRNA, in dorsal root ganglia or trigeminal
 CC neurons. Na_v polypeptides can be obtained by recombinant
 CC expression, and used to treat disorders associated with decreased
 CC sodium channel expression, to screen for compounds that modulate
 CC sodium channel expression or activity, and to raise antibodies
 CC useful as diagnostic agents.
 XX
 SQ Sequence 1765 AA:
 Query Match 88.9%; Score 8153; DB 22; Length 1765;
 Best Local Similarity 88.7%; Pred. No. 0;
 Matches 1569; Conservative 94; Mismatches 99; Indels 6; Gaps 5;
 QY 1 MEERYYPVPPDERNRPFTSDSLAAIKKRTAIQKRRKSKDAAAPQRPOLDKASR 60
 DB 1 meeryypvppdernrfpfdslaaekritiquekkskdaatepqrpqldkasr 60
 QY 61 KLPLKLYGDIPELVTKPLEDLPYKDHKTFMWLNKRTIYRFSAKRALFILGFNPLRS 120
 DB 61 klplklygdvppdliakpliedlpfykdhktfmvlnkrtiyrfsakralfilgfnplrs 120
 QY 121 LMIRISVHSVSMFIICTVIINCMEFMAN--SMERSFNDPIPEYVFIGIYLEAVIKILAR 178
 DB 121 fmrisvhsvsmfiicctviiincmfmanssvdsrpsnipeyvfilyleavikilar 180
 QY 179 GFIVDEFSLRDPNNWLDIVIGTAIATCPGSOV--NLSALRTPRPRALKATISVIGLKL 237
 DB 181 gfvdefsyrdpwnwldivigtaiapcflgnkvnnlstlrtrvralkaisvisgkl 240
 QY 238 VIVGALLRSVKLVDMVWVLTFLCLISFALYQOOLFMGLNOKCIKHNCGPNASNKDCFE 297
 DB 241 vivgallrsvkvldvmvltfclsisfalyqgqlfmgilsgkclkdcdgpnafsnkdcfv 300
 QY 298 KENDSEDFIMCGTWLGRPCPNSTCDKTTLPNDNNYTKFDNFGWSFLAMFRVMTQDSWE 357
 DB 301 kendsedfimcgnwlgrrscpdgstcnktfnpdyntidnfdsgwsflamfrvmtqdswe 360
 QY 358 RLRYQILRTSGIYVFFVFFVWVIFLGSFYLLNLTAVVTMAYEONRNVAATEAKEMFQ 417
 DB 361 klyrqilrtsgyifvffvffviflgsfyllnltlavvtmayeeqnrnvaateakemf 420
 QY 418 EAQOLLREEKALVAMGIDRSSLNLSQASSFSPPKKRFFGSKTRKSFPMRSGKSTAQASAS 477
 DB 421 eaqollreekealvamgidrtsslnlsqassfspkkrffgsktrksfpmrsgskstara 480

QY 1558 QIAVYVSVYIIISFLIVNNYIAVILENFNTATESEDDPLGEDDFEIFYEWKFDPEA 1617
Db 1558 qiaivvsvyiliisflivnnmyiavilenfntateesedplgeddfelfeyiwekfdepa 1617
QY 1618 SOFTQYSALSDFADALEPELRVAKPNKFOFLVMDLPMVMDRLHCMVDLFAFTTRVLGDS 1677
Db 1618 tqfilyeslsdafdalepeplrvaakpnrfqfimmldpmvmdgrlhcndvlfaftrvlgns 1677
QY 1678 SGLDTMKTMEEEKPMEANPKLYEPIVTTTKRKEEQGAAVIQRAYRKHKMKVKLRLLK 1737
Db 1678 sgltdmkameekfmeanpkklyepivtttkrkeeeqaaviqrayrhmkknikiklk 1737
QY 1738 DRSSSHQVFCNGDLSLSDVAKVKVHND 1765
Db 1738 grssssiqvfcngdlsldvpkikhvcd 1765

RESULT 8

AAB20121
ID AAB20121 standard; Protein; 1791 AA.
AC AAB20121;
DT 30-APR-2001 (first entry)
XX Human sodium channel NaN.
DE Sodium channel; NaN; human; tetrodotoxin resistant; pain;
KW paraesthesia; hyperexcitability; analgesic; vaccine; therapy;
KW diagnosis.
OS Homo sapiens.
XX WO200105831-A1.
XX 25-JAN-2001.
XX 14-JUL-2000; 2000WO-US19342.
XX 16-JUL-1999; 99US-0354147.
XX (UYUA) UNIV YALE.
XX Dlb-Hajj S, Waxman SG;
XX WPI; 2001-103147/11.
XX N-PSDB; AAF30101.
XX Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena -
XX Claim 7; Fig 11B; 162pp; English.
XX The present sequence is that of novel human tetrodotoxin resistant sodium channel NaN, as deduced from a cDNA clone (see AAF30101) isolated from human dorsal root ganglia tissue. NaN belongs to the a-subunit/voltage-gated sodium channel protein family. It produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN polypeptides can be obtained by recombinant expression, and used to treat disorders associated with decreased sodium channel expression, to screen for compounds that modulate sodium channel expression or activity, and to raise antibodies useful as diagnostic

QY 929 ETKOLTSPDOGVEMVEFSEDLHLSTQSPRKSDAVSMLESCSTIDILNFRNLQKTVS 988
 Db 952 enktptsqrvqsveidmfdsedephltiqdprkksdvtsilsecstidldqdgfwlpemv- 1010
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 Db 1011 pkqperclpkfgccfpccsvdkrkppwlvwnlrkctqyivkhswfesfiifvillss 1070
 QY 1049 GALLIFEDVNLPSRQVEKLLACTONITFTFLELMILKWNAGFRFRFTSACWDLDELIV 1108
 Db 1071 gallifedvnlpsrqlgclnctdiifhfilemvlkwnagfgyftsawccldfiiv 1130
 QY 1109 VVSLSLMLNPLSLKSFTRLRALRPLRSOPEGMKVVVYALISALPALNLLVCLIFWL 1168
 Db 1131 ivsvttlinlmelsftrlralrplsrfegmkvvvnaligaipalnlvcllfiwl 1190
 QY 1169 VFCILGNVLSFGKRCINGRDINMYLDFTVPMRSOCNITSNYSWKVPQVNFDMGNAYL 1228
 Db 1191 vfcilgyvffsgkfgkclngtd--svinytiitnksqcesgnfswinqkvnfdnvgayl 1248
 QY 1229 ALLQVARYKGLWLETMNAVDSREKDEQDPEANLYAYLVFVFIIFSFTFLNLFIGVII 1288
 Db 1249 allqvarkgwmdliyaavdstekqepetesnlglyfvfviifsgftlnlfigvii 1308
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 Db 1309 dnfoqqkklgqddifnteeqkyynamkklgskkpkpripplnkqgvlfdlvtqsif 1368
 QY 1349 DVIILGILVNLMTMAESADQPKDVKKFTDILNIAFWIFTIECLIKVFAALROHYTNG 1408
 Db 1369 diiisliilnmismaesaynqpkamksilhdlnwfvviftleclikifalrpyyftng 1428
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 Db 1429 wnlfdvvlsvlsvstmlstlengehipfpptlfrvlrlarigrilrvraarigrilf 1488
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 Db 1549 tsagwdslspsmlrskescnss--enchlpgiatyfvsvyililsvlvmymyavilenf 1607
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 Db 1668 lvmdlpmvseidrlhcmdlifaftarvlgsgdldsmkamemekfmeanplkklyepivtt 1727
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 Db 1728 tkrkeergaailqkatrymmkvtkgdqgdqndlenghpsqltclngdlsfvgakg 1787
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 Db 1788 vhd 1791

RESULT 9

AAW23994

ID AAW23994 standard; Protein; 2016 AA.

AC AAW23994;

XX 06-JUL-1998 (first entry)

DT Human hhl sodium channel protein.

XX Ion channel; sodium channel; hhl; human; cardiac cell; heart;

XX pacemaker; gene therapy.

KW

XX Homo sapiens.
 OS WO9802040-A1.
 PN 22-JAN-1998.
 XX 04-APR-1997; 97WO-US05556.
 PF 17-JUL-1996; 96US-0682433.
 PR (MEDT) MEDTRONIC INC.
 PA Morissette J, Stokes KB;
 PI WPI; 1998-110247/10.
 XX N-PSDB; AAV09029.
 DR System for delivering genetic material to heart - comprises
 PT reservoir, catheter and optionally pacing electrode for delivering
 PT ion-channel protein, useful for, e.g. improving sensing by pacemaker
 XX Disclosure; Page 41-47; 73pp; English.
 XX This protein comprises the human hhl voltage-regulated sodium
 CC channel protein that can be used in a novel system for enhancing
 CC cardiac signal sensing by cardiac pacemakers through genetic
 CC treatment. A claimed system for delivering genetic material (GM)
 CC comprises a reservoir containing GM and a device for delivering it
 CC to myocardial cells (MC) at a specific location. The GM increases
 CC the amplitude of the cardiac signal, improving the signal-to-noise
 CC (S/N) ratio that is sensed by the electrode of a pacemaker. Also
 CC claimed are: (1) an implantable delivery system comprising a
 CC reservoir for GM which increases the expression of ion channels in
 CC MC and system for delivering this through a catheter, the tip of
 CC which engages MC at the chosen location, and (2) a system similar
 CC to (1) comprising a pacing electrode on an inner wall of the heart,
 CC close to the site where the GM is delivered. The system is used
 CC for delivery of an ion-channel GM which causes depolarisation of
 CC atrial and ventricular MC and improves the sensing of cardiac
 CC signals by the pacemaker and the S/N ratio of atrial P-waves. The
 CC preferred GM comprises DNA (see AAV09029) or RNA encoding hhl.
 XX Sequence 2016 AA;

Query Match

Best Local Similarity 51.4%; Score 4712.5; DB 19; Length 2016;
 Matches 971; Conservative 281; Mismatches 434; Indels 247; Gaps 29;

QY 15 NFRPFTSDSLAAIKKRIAOKER-----KSKDKAAAEPPRPQDLKASRKLPLKLGDI 69
 Db 12 srrftreslaalekrmaekqargsttlqesreglpeeeaprpqldlqskklpdygnp 71
 QY 70 PPELVTPLEEDLPDYKDKHTFMVNLKRTYRESAKRALFILGFNPNPLRLSLIRISVHS 129
 Db 72 pqligepleddpftstqktfvlhngktrifrsatnalyvspfhpvraraaklvhs 131
 QY 130 VFSMFICTVIINCMFMANSMERSFDNDIP-----EYVFTGIVILEAVIKILARGFTVD 183
 Db 132 lfmnlmctiltncvfma-----qhdppptkyveyftfaiyfeslvkilarafelh 184
 QY 184 EFSFLRDPWNWLDIFVIGTAIATCFPGSQVNLSALRFRFRFRALKALISVLSGLAVIGAL 243
 Db 185 afflrpwnwldfsvlimayttefv-dlgnvsalrfrvrlalktisvsglktivgal 243
 QY 244 LRSVKLLVDVNVLTFLCLSLIFALVGQOLFGLLNOKLKHNCGPNA----- 290
 Db 244 lqsvkkladvmvltvfcslvsfaliqlfmgnlrhkvrnftalngtngsveadglvves 303
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 Db 304 ldylsdpnyllkngtsvllcngssdagtcpegycclkagenpdbhgtsfdfsawaf1 363

QY 346 AMFRVMTQDSWERYLYROILRTSGIYFVFFVVFVIFLGSFYLLNLTLAVVTMAYEEQNRNV 405
Db 364 alfrlmtqdcwerlyqqltsagklymiffmlvflgsfylvnlilavvamaeyeeqat 423
QY 406 AAEATEAKEMFOEAQOQLLREEKALVAMGDRSLNSLOASSFSP-----KKRFFG 457
Db 424 laeteekkrfqaemllkhealtirgvdtsrslslemplapvnsherrskrms 483
QY 458 S-----KTRKS-----FFMRGSKTAQASA 476
Db 484 sgteecgedrlpksdsedgprammhlsltrglrtsmkprssrgsiftfrirdlgseadf 543
QY 477 DSDEDDASKN-----POLLEQTKRLSQNLPL----- 501
Db 544 addenstareshtallvwpplrtsagqpgpptsagphalhghkknstvdngvvs1 603
QY 502 -----VDLDFDEHVDPLHRQ 515
Db 604 lsgedpatspgshllrpvmlehpddttptseepggpmlltsqapcvdvgfee---pgarq 660
QY 516 RALSASILRITTOEQEKFOEPFPCGKNLASKYLVWDCSPQWLCIRKVLRTIMTDPFTE 575
Db 661 ralsavsultsaleeleeshkpcpcwnrlaqryliwecplwmsikgqkvlvmdpftd 720
QY 576 LATIICIIINVTFLAVEHNNMDDNLTKILIGNWVFTGIFTAEMCLKIIALDPPHYPRHG 635
Db 721 ltitlmcivlntlfmalehymntsefeemlvgnlvfegiftaentfkialldpvyfyqg 780
QY 636 WNVFDSIVALLSLADVLYNTLSDNNRSLASLRVLRVEKLAKSWPTLNTLKIIGHSVGA 695
Db 781 wnlfdslvilsimelglsms--nlsvlrfrllrvfklsakswptlntliklignsvga 838
QY 696 LGNLTVTTLTVTFVIFSVVGRMLFGTKFNKATAYATQERPRRRHMDNFVHSLVVRILCG 755
Db 839 lgnltvlalvifvavmgqlfgknyseir-dsdsllprwhmdffhafiifrilcg 897
QY 756 EWENMMGQMDQDGPCLCIIVFVLMVIGKLVNLFIALNLNSFNEEKDGSLEGETR 815
Db 898 ewletmwdcm-evsgqslcllvflvmvignlvnlflallssfsadnltapde-dre 955
QY 816 KTKVQLALDRFRRAFSFWLHALQSFCCCKCRK-----NSRPKE 855
Db 956 mnnlqalalrigrfrvtrttwdfccglhrhrpqkpealaagqqlpsciatpysppppe 1015
QY 856 TTESFAGENKDSILPDRAPKKEYDTDMALVTGOAGAPLA---PLAEVEDDV--EYCGEGG 910
Db 1016 tek-----vpptrketqfeegqpggtpgdpdvcvplavaesdtdddeeden 1065
QY 911 ALPTSQHSAGVQAGDL-----PPETK---QLTSPDQGVEMEVFSEEDLH-----LSIQ 956
Db 1066 slgteesskqesqpsvsgwprgppdsrtwsqvsatasaeasea-sqadwrgqwkapeq 1124
QY 957 SPRKSDAVSMLSCSTIDLN---DIFRNLOKTVSPKQDPRCPKGLSCHFLCHKTKDR 1013
Db 1125 apgctepdscsgestadntntaelleqldlgdqvdkpbedcftegcvrrcpocavdt 1184
QY 1014 KSPWLVWNNIRKTCYQIVKHWSPESTFIIFVILLSSGALIFEDVNLPSRPOVEKLLRCTDN 1073
Db 1185 qagqkvwrirktcyhiveshwfcfifmllssgalafedyleerktikvllayadk 1244
QY 1074 IFTFIFLLEMLKWAFAFRFRYETSAMCWLDFLIVVVVLSLM-----NLPSLKSFRT 1126
Db 1245 mftyvfvlemlkvwavgyfkfytanawcwidflivdsvlsvalntlgfaemgpikslrt 1304
QY 1127 LRALRPRALSQPRGMKVYVALISAPILNVLVLCIFLWVFCILGVNLFSGKFGRCI 1186
Db 1305 lralrpralsrfegmrvvvnalvgalpsimnvlvcilfwlflsimgvnlfaqkfgrci 1364
QY 1187 NGTDINMYLDFTEVPNSQCNISYS---WKVPQVNFNDVGNAYLALLOVATYKGLLEI 1242
Db 1365 nqtegdplnnytnvnksqcsnltgelywtkvkvnfnvngagylallqvatkfwmdl 1424

QY 1243 MNAADVDSREKDEQDPFEANLYAYLYFVVFIFIGSFFTLNLFIGVINDFNQOQKKLGQD 1302
Db 1425 myaadvrgyeeqppqweynlymylyfyfifligsfctlnlfigvldnfqqkklqggd 1484
QY 1303 IFWTEEQKKYNNAMKLGTKKPKQPIRPLNKKCAFVFDLVTQVDFVILGLLVLNMI 1362
Db 1485 lfmteeqdkkynamkkgkpkpripnkpyqgffidvktqafdvtfmflclomvt 1544
QY 1363 MMAESADQPKDVKKTFDILNIAFVITIECLIKVFALRQHYFTNGWNLFCVWVLSII 1422
Db 1545 mmvetddqspekinilakinllfvaiftgecivklaalrhyfftnsnwifdfvfvvlisiv 1604
QY 1423 STLVSRLSDSDISPPPTLFRVRLARIGRLRLVRAARGIRTLFALMMSLPSLFNIGLL 1482
Db 1605 gtvlslidliqk-yffsptlfrvrlarigrilrlirgagkirtllfalmslpalfnigl 1663
QY 1483 LFLVMFVIAIYFGSMFVKVKGSGIDIDFNFETFTGSMCLCLOITTSAGNDTLLNPMLE- 1541
Db 1664 lflvmflysifgmfanfaykvkweagiddmfqtfansmclcfqittsagwogllsplnt 1723
QY 1542 AKEHC-----NSSSDSCQOQPIAVVYFVSIIISILVVMYIAVILENFNTATEESE 1595
Db 1724 gppycdptlpnsngsrgdcgspavgilfftyliisfliivmnyiailenfsvateest 1783
QY 1596 DPLGEDDFEIFYEWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKFOFLVMDLPMV 1655
Db 1784 eplseddfmfeiwefkfdpeatqfeyvsldfadalseplriakpnqislmndipmv 1843
QY 1656 MGDRLHGMVLFATFTRVLGDSGLDMKTMMEKEKEANPFKLYEPITVTTTKRKEEQ 1715
Db 1844 sgdrfchmdlfaftkrvlgsengemdalkiqmeekfmaanpskisyepittttrrkheev 1903
QY 1716 GAAVIQIRAYRKHM 1728
Db 1904 samviqrafrhl 1916

RESULT 10

AAB82242

ID AAB82242 standard; Protein; 2015 AA.

XX AAB82242;

XX 21-JUN-2001 (first entry)

XX Human SCN5A mutant delf1617.

XX SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy;
KW drug screening; mutant; mutein.

OS Homo sapiens.

XX WO200124681-A2.

XX 12-APR-2001.

XX 09-AUG-2000; 2000WO-US21660.

XX 09-AUG-1999; 9905-0147488.

XX 17-MAR-2000; 2000US-0190057.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Splawski I;

XX WPI; 2001-290564/30.

XX New KVLQ1 and SCN5A genes, which contains alterations or mutations,

PT useful in diagnostic/prognostic or drug screening methods, particularly
PT in mutational analyses for screening individuals with or at risk for
XX long QT syndrome

Claim 31; Page -; 76pp; English.

The present sequence is that of the claimed delF1617 mutant of the human SCN5A protein. The mutant is encoded by an SCN5A mutant gene carrying a deletion of the TTC codon for phe-1617. Mutations of the SCN5A gene are implicated in Romano-Ward syndrome, the autosomal dominant form of Long QT syndrome (LQTS). Mutations newly discovered in the SCN5A gene lead to the following amino acid alterations in the encoded protein: D1114N, L1501V, delF1617, R1623L, E1784K and S1797N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCN5A gene. Note: the present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing (see A8B82220).

Sequence	2015 AA;
SQ	

Sequence	2015 AA;
SQ	

Query Match 51.4%; Score 4712; DB 22; Length 2015;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 972; Conservative 280; Mismatches 430; Indels 254; Gaps 30;

QY	15	NFRPFTSDSLAAIKKRIAQKER-----KKSKDKAAAEPPQRPQDLKASRKLPKLYGDI	69
		: : :	
Db	12	sfrrfreslaalekmaeqkqrgsttlqgesregipeeeearpqldlgaskllpdjgnp	71
		: : :	
QY	70	PPELVTKPLEDDPPYKDHKTMVLNKKKTIYRFSAKRALFTILGDPNPLRLSLMIRISVHS	129
		: : :	
Db	72	pqeliegpedlpprystdktfivlnkgtklfrsatnalyvshpvrreaavkllvhs	131
		: : :	
QY	130	VFSNFICTVIINCMEFANSMERFSNDIP-----EYFVIGIYILEAVIKILARGFIVD	183
		: : :	
Db	132	lfmllmctaltncvema-----qhdppwtkyeyftaiytfesivkkrarafeclh	184
		: : :	
QY	184	EFSLRDPNNWLDPIVIGTAITCFPGSQVNLSALRTFRVRALKAKAISVISCKVIVGAL	243
		: : :	
Db	185	aftllrdpwnldfsvilmayttefvl-dlgnvsalrtfrvlralktisvisgltktivgal	243
		: : :	
QY	244	LRGSKVLVDVMVLTFLCSLTFALVGQOLPMGILNOKCIKHNGGNPAA-----	290
		: : :	
Db	244	iqgsvkkladvmvltvclsvfaligqlfmgnlrhkcvrnfaltngtngsveadglvws	303
		: : :	
QY	291	-----SNKDCFEKEKDESEDFIMCGTWLGRSPNGSTCDKTTINPDNNYTKFDNFGWSFL	345
		: : :	
Db	304	ldlylsdpenylikngtsdvlvcgnssdagtcpegycrlkagenpdhgytsfdfsawaf	363
		: : :	
QY	346	AMFRVMTQDSWERLYQRIILTSGIYVFVFVVIFLGSFYLLNLTLAVVMTMAYEBSQNRV	405
		: : :	
Db	364	alfrlntqdcwerlyqtrlsagkiymifmivflglsfylnllavvmaeyesqndat	423
		: : :	
QY	406	AAETEAKEMFOBAQOLLRREKEALVAMGIDRSSLNSLOASFSF-----KKRKFFG	457
		: : :	
Db	424	iaeteekrfqeamelkhealrtirgvtvtsrsslmslapvsherrtskrkrkms	483
		: : :	
QY	458	S-----KTRKS-----PFMRGSKTAQASA	476
		: : :	
Db	484	sgteecegdrlpkdsedegpramnhlsrlgrlsrtemkprsrgrsiffrldlgsedaf	543
		: : :	
QY	477	SDSEDDASKN-----POLLEQTKRLSNLP-----	501
		: : :	
Db	544	addenstareshtslvlpwplrrtsaqgqpspgtsapghalhgkknstvdvcngvysl	603
		: : :	
QY	502	-----VDLFDEHDVPLHRQ	515
		: : :	
Db	604	lgagdbeatspgshllrprvmlehpdtttpseepgpgmltsqapcvdgdfee-----pgarq	660
		: : :	
QY	516	RALSAYSILTIITIOEQEFQECFCPGKNLASKYLVWDCSPOWLCTIKKVLRTIMTDPDTE	575
		: : :	
Db	661	raisavsvltsaleeleesrhkcpccwnlagryliwecpcplwmslkggvgklvnmdbptd	720
		: : :	
QY	576	LATITCIINTVFLAVEHNMDDNLTILKIGNVFTGIFIAEMCLKIIALDPYHVRHG	635


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Db 1125 apgcgetpedscegstadmntaelleq:lpdlqgdkvdpbedcftegcvrrcpccavdtt 1184
Qy 1014 KSPVWLVNWNIRKTCYQVVKHSWPSFIFVILLSSGALIFPDVNLPSRPQVEKLLRCTDN 1073
Db 1185 qapgvwvrrlkrctchiveshswfctifimillssgalafediyleerktikvilevadk 1244
Qy 1074 IFTFIELLEMLKVVAFGEFRYFTSAMCWLDLFLVVVSLM-----NLPCLKSPRT 1126
Db 1245 mftyvylemlkvwaygfkfynawcwldflivdvslsvlantlfgaemgpikslrt 1304
Qy 1127 LRALRPLRALSOFGMKVYVVALISAIPAILNVLVLCILFWLFCILGNLFSKFGRCI 1186
Db 1305 lralrplralrsefegmrvvvalgaipsimvllcelfwlifsimgnvlfagkfgrci 1364
Qy 1187 NGTDINMYLDFTEVPNSOCNISNYS-----WKVQVNFNDVGNAYLALLQVATYKGLWEI 1242
Db 1365 nqtegdiplnytlvnmksqcesnlgtelywtkvkvfnvfnvgagyallqvattfkvgvmdi 1424
Qy 1243 MNAAVDSREKDEOPDFEANYLYAYLYFVVVFIIFGSEFTLNLFIQVVIDNFNOQOKKIGQD 1302
Db 1425 myaavdsrgyeedqpwynlymylyfviifigsfftnlfigvliidnfnqgkkkl99qd 1484
Qy 1303 IFMTEQKKYYNAMKLGTKPKQPIPRPLNKCQAFVFDLVTQVDFVILGLILVNLNII 1362
Db 1485 ifmteeqkyynamkkgkpkqpiprlnkyqgfidvktqafvtimfliclmvt 1544
Qy 1363 MNAESAQPKDKVKTFDILNIAFVFTIECLIKVFALRQHYFTNGNLFDCVVVLSII 1422
Db 1545 mnvetddqspekinilaklnlifaiftgecivkialrhyffnswnifdvfvvilsiv 1604
Qy 1423 STLVSRLSDSDISPPPTLFRVRLRIGRILRLVRAARGIRTLFALMMSLPSLFNTGLL 1482
Db 1605 gtvisldiqk-yffsptlfrvirarigrilrigrakgrtlifalmslpalfn.9ll 1663
Qy 1483 LFLVMFYIAIFGMSWFSKVKKGSGIDDIFNFTFTGSMCLCFQITTSAGWDTLNPMLE- 1541
Db 1664 lflvmfisyifgmanfaykvweagiddmfnftqfnsmlclcfqittsagwdglisplnt 1723
Qy 1542 AKEHC-----NSSQSDSQOQIATVYFVSYIIISLIVVMYIAVILENFNTATESE 1595
Db 1724 gpyyctplnpsngsrdcsdpavglifttyiisflivnmvialilensfateest 1783
Qy 1596 DPLGEDFEIYEWKEXFDPEASOFIOVSALSDFADALPEPLRVAKNKFOLFVMDLPMV 1655
Db 1784 eplsedfdmfeiwefkdfpeatfiesvlsdfadalseplriakpnqislinmdlpmv 1843
Qy 1656 MGDRLHCHMDVLFATTTVLGDSGLDTMTKMTMEKFMFANPKKLYEPVITVTTTKRKEEQ 1715
Db 1844 sgdrichmdilfaftkrvlgesgemdalkiqmeekfmaanspkisyepitttlrrkheev 1903
Qy 1716 GAAVIQRAYRKH 1728
Db 1904 samviqrafrhl 1916
```

RESULT 12

AAB82240
ID AAB82240 standard; Protein; 2016 AA.

AC AAB82240;

XX 21-JUN-2001 (first entry)

DT Human SCN5A mutant D1114N.

XX SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy;
KW drug screening; mutant; muten.

OS Homo sapiens.

XX W0200124681-A2.

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XX 12-APR-2001.
PD 09-AUG-2000; 2000WO-US21660.
XX 09-AUG-1999; 99US-0147488.
PR 17-MAR-2000; 2000US-0190057.
XX (UTAH ) UNIV UTAH RES FOUND.
PA Keating MT, Splawski I;
XX WPI; 2001-290564/30.
XX New KVLQT1 and SCN5A genes, which contains alterations or mutations,
XX useful in diagnostic/prognostic or drug screening methods, particularly
XX in mutational analyses for screening individuals with or at risk for
XX long QT syndrome
XX Claim 31; Page -; 76pp; English.
XX The present sequence is that of the claimed D1114N mutant of the
XX human SCN5A protein. The mutant is encoded by an SCN5A mutant
XX gene in which a G/A mutation alters codon 1114 from GAC to AAC.
XX Mutations of the SCN5A gene are implicated in Romano-Ward syndrome,
XX the autosomal dominant form of Long QT syndrome (LQTS). Mutations
XX newly discovered in the SCN5A gene lead to the following amino acid
XX alterations in the encoded protein: D1114N, L1501V, delF1617,
XX R1623I, E1784K and S1787N. Knowledge of the mutations provides
XX means for assessing a risk in a human subject for LQTS, for
XX diagnosing a mutation which causes LQTS, and for screening for drugs
XX useful in treating a human having a mutation in the SCN5A gene.
XX Note: The present sequence is not shown in the specification but is
XX derived from the KVLQT-1 sequence given in the Sequence Listing
XX (see AAB82220).
```

CC Sequence 2016 AA;

Query Match 51.48; Score 4711.5; DB 22; Length 2016;
Best Local Similarity 50.18; Pred. No. 0;
Matches 970; Conservative 279; Mismatches 433; Indels 255; Gaps 28;

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Qy 15 NFRPETSLSLAAIKKRTAIOKER-----KSKDKAAAEPPQRPOLDLKASRLKPLKYGDI 69
Db 12 sfrffreslaalekmaekqargsttlqesreglbeeeaprpqldlqaskklplygnp 71
Qy 70 PPELVTPLELDPPYKDKHTFMVLNKKRTIYFESAKRALFILGFNPLRLSIRISVHS 129
Db 72 pqeligepleddpfystqktfivlnkgktifrsatnalyvlsfpfpvrraavkllvhs 131
Qy 130 VFSMFICTVTIINCFMANSMEERSFDNDIP-----EYVFTGIYILBAVILARGFTVD 183
Db 132 lfnmlimctiltncvfma-----qhdppptkyveyftfaiytfeslvkilarafclh 184
Qy 184 EFSELRDPWNWLDPIVIGTAITATCFPGSQVNLSALRFRFRERALKATSVISGLAVIVGAL 243
Db 185 aftflrdpwnwldfsvlimayttefv-dlgnvsalrtrfvralktisvisgltivgal 243
Qy 244 LRSVKLVDMVNLTLFCLSLIFALVGQQLFMGLNOKCKIKHNGCPNPA----- 290
Db 244 lqsvkkladmvtlvcfclsvfaliglqlfmgnlrhkvrnftalngtngsveadglvwes 303
Qy 291 -----SNKDCFEKEKDESDFTIMCQTLWLSRCPNGSTCDKTTLNDNNYTKFDNFGWSFL 345
Db 304 ldlvlsdpenyllkngtsdvllcgnssdagtcpegycclkgapndhgytfsdfsawaf 363
Qy 346 AMFRVMTQDSWERLYRQILRTSGIYFFVFFVWVIFLGSFYLLNLTLAVTWMAYEQNRNV 405
Db 364 alfrimtcqdwerylqgltlrsagkiymflmvlifslfylnlilavvamayeegnat 423
Qy 406 AAETEAKEMFQEAQQLLREKEALVAMGIDRSSLSNLQASSFSF-----KKRKFFG 457
Db 457
```

Db 424 iaeteekrfqeamemlkhealtirgvdtsrslslemplavpnsherrkrkms 483
Qy 458 S-----KTRKS-----PFMRGSKTAQASA 476
Db 484 sgteecgedrpkdsedgpramhhlsltrglsrsmkprssrgsiffrirdlgseadf 543
Qy 477 SDESDASKN-----POLLEOTKRLSONLP----- 501
Db 544 addenstareshhtslvpwrrtsaqgpgstsapghalhgnknstvdngvvs1 603
Qy 502 -----VDLFEHVDPLHRQ 515
Db 604 lgaedpeatspgshllrpvmlehpddtttseepgpgmltsqapcvdfee---pgar 660
Qy 516 RALSAVSILTTIOEQKRFQPCPCGKNLASKYLWDCSPQWLCKIKVLRTIMTDPRTE 575
Db 661 raleavsvltaleeeshrkpcpcwnrlaqryliwecclwmsikgvgklvmdpftd 720
Qy 576 LAYTICIINTVFLAVEHHNDDNLKTLTKIGNWVFTGIFTAECLKIIALDPVHYFRHG 635
Db 721 ltimcivlntifmalehymntseemlvgnlvftgftaentfkialdpvvyfqq 780
Qy 636 WNVDSIVALLSLADVLYNTLSDNRSFLASLRVLFKLSKSWPTLTLKIIGHSGVA 695
Db 781 wniidsiivlismelglsrms--nlsvlrfrlrvfklakswptntlikilgnsvga 838
Qy 696 LGNLTVLTIVVFISFVVMRLFGTKFNKTATAYATQERPRRRHMDNFVHSLVVFRLCG 755
Db 839 lgnltvlavilfivavgmglfknyselr-dsdgllprwhmdffhafiifrlcg 897
Qy 756 EWENMGCMODGSPICIIIFVILIMVIGKVLNLFIALLLNSFSNEEKDGLSEETR 815
Db 898 ewietmwdcm-evsgqslcllflvmvignlvlnflallssfaadnltapde-dre 955
Qy 816 KTKVQLADRRFRFAFSLMHLAQSCCKCKRK-----NSPKRKE 855
Db 956 mnnlqalarlqrglrkrtdwtfcgllhrpqpaalaaqgqlpsciatpysppppe 1015
Qy 856 TTESFAGENKDSILDPARPKKEYDTDMALYTGQAGAP---LAPLAEVEDDY--EYCGGG 910
Db 1016 tek-----vpptketeqeeqpgggtgdpvcpvpiavaesdtddeeden 1065
Qy 911 ALPTSQHSAGVQAGDL-----PPTKQLTSDDQGVEMVEFSEEDLHLS----- 954
Db 1066 slgteesskqdesqpgvsgwprgppdstwtswq-----vsatasaeasasqanwrgqwk 1120
Qy 955 --IOSPKKSDAVMSLSCSTIDLN---DIFRNLOKTVSPKKQDPDRCPFKGLSCHFLCHK 1009
Db 1121 aepqagcgetpedscesgscadmtntaelleqldlgdvkdpcedctgcvcrrcpcca 1180
Qy 1010 TDKRKSPVWLWNIRKTCYQIVKHSWFESFIIFVILISSGALIFEDVNLPSRPQVEKLLR 1069
Db 1181 vdtqagpkvwwlrktcyhivshswfetfiifmllssgalafedylearktkikville 1240
Qy 1070 CTDNIETFIPLLEMLKWAFFGRYFTSAWCWLDLFLIVVVSLSM-----NLPSLK 1122
Db 1241 yadkmftyvfvlemlkwwavgyfkfncawcldflivdvslvslvantlgfaempik 1300
Qy 1123 SFRTLRALRPLRALSGEKMVVVYALISAPAILNVLVCLIFWLFCILGVNLFSGKF 1182
Db 1301 slrtlrplralrslrtegmrvvvvvalvgaipsmrvllvclflwifslmgvlnfagkf 1360
Qy 1183 GRCINGTDINMYLDFTVPRNSOCNISNYS----WKVPQVNFNDVGNAYLALLOVATYKG 1238
Db 1361 grcinqtegdplpnytlvnnksqesnlgtelywtkvkvfnvndvgaaylallqvattkg 1420
Qy 1239 WLEIMNAVDSREKDEQDFEALNYAYLYFYVFIIFGFFTLNLFIVGIIIDNFQOQKKL 1298
Db 1421 wmdlmyaavdrgyeegqpweynlymylyfviifigsfflnlfigviidnfnqgkkl 1480
Qy 1299 GGQDIFTEEQKYYNAMKLGTKPKQPIPRPLNKCQAFVDLVTSQVDFVILGLLVL 1358
Db 1481 gggd1fmeteeqkyyenamkkgkpgkplprpnkygffidvktqadvtimflicl 1540

Qy 1359 NMIIMAESADQPKDVKKTFDILNIAFYVFIETIECLIKVFALRQHIFTNGNLFDCVVVV 1418
Db 1541 nmvmvmetddqgspeknilakinllvaiftgecivklaalrhyyftcnswnifdvv1 1600
Qy 1419 LSIISTLVSRLESDISFPPTPLFRVVRRLARIGRLRLVRAARGIRTLFALMMSLPSLNF 1478
Db 1601 lsiivgtvlsdlqk-yffsptlfrvirirgrirgagkirtlilfalmmalpalfn 1659
Qy 1479 IGLLFLVMFIYALFGMSWFSKVGSGIDIDIFENFETGTGSMCLCFQITTSAGWDTLLNP 1538
Db 1660 iglllflvmfiyslfgmanfayvkweagiddmfntqtfansmclcfqittsagwdgllsp 1719
Qy 1539 MLE-AKEH-----NSSSDSCSQOQIAVYVFSYIIISFLIVVMYIAVILENFNAT 1591
Db 1720 ilntgppycdplnpsngsrgdcgspavgllfttyiisflivvmyiaillenfsat 1779
Qy 1592 EESDPLGEDFEIFYEWKFDPEASQFIQYSALSDFADALPEPLRVAKPNKQFLVMD 1651
Db 1780 eestplseddfmfyeiwekfdeatfleysvlsdfadalseplriakpnqislimd 1839
Qy 1652 LPMVMGDRLHCHMDVLFAFTTRVLGDSGLDTMKTMMEEKFMEANPFKLYEPITVTTKRK 1711
Db 1840 lpmvsgdrhchmdlifaftkrvlgesgemdaikimeekfmaanspkisyepitttlrkr 1899
Qy 1712 EEEQGAAYIQRAYRKHM 1728
Db 1900 heevsamvigrfrrhl 1916

RESULT 13

AAB82245

ID AAB82245 standard; Protein; 2016 AA.

XX AAB82245;

XX 21-JUN-2001 (first entry)

XX Human SCN5A mutant S1787N.

XX SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
XX Romano-Ward syndrome; diagnosis; prognosis; therapy;
XX drug screening; mutant; muten.
XX Homo sapiens.

XX WO200124581 A2.

XX 12-APR-2001.

XX 09-AUG-2000; 2000WO-US21660.

XX 09-AUG-1999; 99US-0147488.

XX 17-MAR-2000; 2000US-0190057.

XX (UTAH) UNIV UTAH RES FOUND.

XX Keating MT, Splawski I;

XX WPI; 2001-290564/30.

XX New KVLQTL and SCN5A genes, which contains alterations or mutations,
XX useful in diagnostic/prognostic or drug screening methods, particularly
XX in mutational analyses for screening individuals with or at risk for
XX long QT syndrome

XX Claim 31; Page -, 76pp; English.

XX The present sequence is that of the claimed S1787N mutant of the
XX human SCN5A protein. The mutant is encoded by an SCN5A mutant
XX gene in which a G/A mutation alters codon 1787 from AGT to AAT.
XX Mutations of the SCN5A gene are implicated in Romano-Ward syndrome,
XX the autosomal dominant form of Long QT syndrome (LQTS). Mutations

newly discovered in the SCNSA gene lead to the following amino acid alterations in the encoded protein. D1114N, L1501V, delF1617, R1623L, E1704K and S1787N. Knowledge of the mutations provides means for assessing a risk in a human subject for LQTS, for diagnosing a mutation which causes LQTS, and for screening for drugs useful in treating a human having a mutation in the SCNSA gene. Note: The present sequence is not shown in the specification but is derived from the KVLQT-1 sequence given in the Sequence Listing (see AAB82220).

Sequence 2016 AA;

Query Match 51.4%; Score 4711.5; DB 22; Length 2016;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 970; Conservative 281; Mismatches 435; Indels 247; Gaps 29;

QY	15	NFRPFTSDSLAATKRIAIOKER-----KKSOKAAAEPOPRQLDULAKSRKLPUKYGDI	69
Db	11	: :	70
Db	12	sfrftrteslaaeikmaeqgargsttlqesreglpbeeeaprqldlqaskklpdlygnp	71
QY	70	pPELVTPLEDDLPYYKDKHTEVMVLANKKRTIYRFESAKRALFLILGPENRSLMRISVHS	129
Db	11	: :	130
Db	72	pqeiligepldqpystqtffvlnkgtkiffsatunalyvspnhpvravaakvlivs	131
QY	130	VFSFIITCIINIEMANSWERSFONDIP-----EYVFIGIVILEAVIKILARGFIYD	183
Db	132	lfmalmctiltncvfma-----qhdpptwkyyeyftfaiytfeslvkilarafclh	184
QY	184	EFSFLRPWNWLDFIVIGTATAICTFCPSQVNLSALRTFRVRALKAIASVISGLKVIUGAL	243
Db	185	aftiridpwnldfsvilmayttefv-dlgnvsalrtfrvrlalkisvisglktivgal	243
QY	244	LRSVKVLVDVMVTLFCLSFIFALVGQOLFIMLQNKICKHNCGNPNA-----	290
Db	244	iqsvkkiladvmtvtvfcslvfalgqlfgnmlrhkcvrnfntalngtngsveadgilwes	303
QY	291	-----SNKDCFEKEKSEDFIMCGTWLGSRPCNGSTCDKTTLNPNNTYTKFDNFGWSFL	345
Db	304	ldylsdpenyllknngtsdvllcgnssdagtcpegryclrkagendphgytsdfsawafil	363
QY	346	AMPRVTMTQDSWERLYROILRTSGIYFFVPFVVVIFLGSFYLLNLTVAVTMAYEEQNRV	405
Db	364	alfirmicqdwerlyqqclrtasagiymiflmflvfigsfyvnlitavvameyeengnat	423
QY	406	AAETEAREKMFOEAQQLLREEKALYAMGIDRSSLSLAQASSFP-----KKRKFFG	457
Db	424	iaeteekefrqeamemlkkehealtirgvdytvrsrslmsplayvnsherrskrrkms	483
QY	458	S-----KTRKS-----PFMRGSKTTAQASA	476
Db	484	sgteecgedrpkdsdsedgprannhisltrglrtsmkprsrsgiftfrrdlgseadf	543
QY	477	SDSEDDASKN-----POLLEOTKRLSQNL-----	501
Db	544	addenstareshtseltvpwplrirtsadgspsgtsetagghalhokkstvdncgvsl	603
QY	502	-----VDLFDEHVDPHLHQ	515
Db	604	lgagdpeatpgshllrpvmlehpddttiseepgpqmitsaqpcvdfee--pgarq	660
QY	516	RALSAYSILITTOEQEKFOEPFCCKKNLASKYLWDSCPWMLCTCKKVLRITMTDPPTE	575
Db	661	ralsavsylvlsaleeletesrhkcoppownrlaqryliweccplwmiskggkvklvmpdfid	720
QY	576	LAITICIIINTVFLAVEHHNMNDNLKTILIGNWVTFGIASCMUKLIALLDPHYHFHG	635
Db	721	ltitmciivntlmeahyntmetsefeemlqvgnlvfigiftaemtfkialdpvyfyfqg	780
QY	636	WNVPDSTIVALLSADVLYNTLSNNRSFTLASRLVRFKLAKSWPTLTNTLIKIHGSVA	695
Db	781	wnfidslivalsimelglsrms-nlsvlrtsfllrvfkwlakswwptintlikignsva	838


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Qy 1074 IFTFTLEMLTKVAFGRFERYFSAMCWLDFLIIVVSVLSIM-----NLPSLKSPRT 1126
Db 1245 mftyvfvlemllkwvaygfkfynacwcllvdvslvsvantlgfaemgpikslrt 1304
Qy 1127 LRALRPLRALSQFEGMKVYVYALISAIPAINLVLLVCLIFWLVFCILGVNLFSGKFGRCI 1186
Db 1305 LRALRPLRALSRFEGMRVNVNALGALPSIMNVLLVCLIFWLVFCILGVNLFSGKFGRCI 1364
Qy 1187 NGTDINMYLDTFVNPQRSCNINYS-----WKVPOVNFNVGNAYLALQVATYKGMLEI 1242
Db 1365 nqtegdplnytiwnksqcslnltgelywtkvkvnfdnvgagyallvqatfkqwmidi 1424
Qy 1243 MNAADVSRKDEQDPDFEALNAYLYFVVFIFIGSFFTLNLFIGVIIDNFNOQKKLGQD 1302
Db 1425 myaavdsrgyeegpqweynlymyfyvfiifigsfntlnlfignldnfnqgkklgqgd 1484
Qy 1303 IFMTEQKYYNAMKKLGTRKPKQPIPRPLNKCQAFVDFLVTQVDFVILGLIVLNMI 1362
Db 1485 ifmteeqkyyNAMKKGSKPKQPIPRPLNKCQAFVDFLVTQVDFVILGLIVLNMI 1544
Qy 1363 MNAASQPKDKVKTFTDILNFAVFIETIECLIKVFAIRQHYFTNGWNLFCVYVVLISII 1422
Db 1545 mmvetddgspekinilaklnllvaiftgecivklaalrhyftnwnfnifdvvvlisv 1604
Qy 1423 STLVSRLSDSDISPPPTLFRVRLARIGRLRLVRAARGITLIFALMMSLPSLFNIGLL 1482
Db 1605 gtvlsldliq-yfssptlfrviriarigrilrlrgakgrtllfalmmslpalnagll 1663
Qy 1483 LFLVMFIYAFGMSWFSKVKSGSGIDDIFFNPFTTGSMLCLFQITTSAGWDTLLNPMLE- 1541
Db 1664 lflvmfiysifgmanfaykveagidmfnfqtfansmclcfqittsagwdgllspint 1723
Qy 1542 AKEHC-----NSSQSDSCQOQIAVYFVSYIIISFLVNVNMYIAVILENFTATESE 1595
Db 1724 gpycydptlpnsngsrgdspavgilfftyiisflivnmyiaailenfsfateest 1783
Qy 1596 DPLGEDDFEIFYEWEKEDPEASOFIOYSALSDFADALPEPLRVAKNPKFQVLDLPMV 1655
Db 1784 episeddfdmfyeiwekrdpeatgfiesvlsdfadalsepilrlakpnqislinmdlpmv 1843
Qy 1656 MGDRLHCHMDVLFAPTRTVRLGDSGLDTMTKMTWMEKFMWEPFKKLYEPIVTTTKRKEEQ 1715
Db 1844 sgdrhcmddilfatkrvlgesgemdalkiqmeekfmaanspskisyepitttlrrkheev 1903
Qy 1716 GAAVQIRAYRKHM 1728
Db 1904 samvigrarrrhl 1916

RESULT 15
AAB82244
ID AAB82244 standard; Protein; 2016 AA.
XX
AC AAB82244;
XX
XX 21-JUN-2001 (first entry)
XX
DE Human SCN5A mutant E1784K.
KW SCN5A; Long QT syndrome; LQTS; cardiovascular disease;
KW Romano-Ward syndrome; diagnosis; prognosis; therapy;
KW drug screening; mutant; mutain.
XX
OS Homo sapiens.
XX
PN WO200124681-A2.
XX
PD 12-APR-2001.
XX
PF 09-AUG-2000; 2000WO-US21660.
XX
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09-AUG-1999; 99US-0147488.
17-MAR-2000; 2000US-0190057.
(UTAH ) UNIV UTAH RES FOUND.
Keating MT, Splawski I;
WPI; 2001-290564/30.
New KVLQ1 and SCN5A genes, which contains alterations or mutations,
useful in diagnostic/prognostic or drug screening methods, particularly
in mutational analyses for screening individuals with or at risk for
long QT syndrome
Claim 31; Page -: 76pp; English.
The present sequence is that of the claimed E1784K mutant of the
human SCN5A protein. The mutant is encoded by an SCN5A mutant
gene in which a G/A mutation alters codon 1784 from GAG to AAG.
Mutations of the SCN5A gene are implicated in Romano-Ward syndrome,
the autosomal dominant form of long QT syndrome (LQTS). Mutations
newly discovered in the SCN5A gene lead to the following amino acid
alterations in the encoded protein: D1114N, L1501V, delF1617,
R1623L, E1784K and S1787N. Knowledge of the mutations provides
means for assessing a risk in a human subject for LQTS, for
diagnosing a mutation which causes LQTS, and for screening for drugs
useful in treating a human having a mutation in the SCN5A gene.
Note: The present sequence is not shown in the specification but is
derived from the KVLQ1-1 sequence given in the Sequence Listing
(see AAB82220).
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SQ Sequence 2016 AA;

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Query Match 51.3%; Score 4708.5; DB 22; Length 2016;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 970; Conservative 280; Mismatches 436; Indels 247; Gaps 29;
Qy 15 NFRFTSDSLAAIKKRTAIQKER-----KSKDKAAAEPPQRPQDLKASRKLKLYGDI 69
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Qy 70 PPELVTPKPLEDDPYKDKHTFMVNLKRTIYREFSAKRALFILGFENPRLSRILTRISVHS 129
Db 72 pqeligepleddpfystqktfvlngkgtlfrfsatnalyvspfpvrraavkilvhs 131
Qy 130 VFSMFIITCTVIINCMFMANSMERSFDNDIP-----EYVFIGIYLEAVIKILARGFTVD 183
Db 132 lfnmlimctiitncvfma-----qhdppptkyveytftaiytfeslvkilarafclh 184
Qy 184 EFSFLRDPWNWLDIFIVIGTAIATCFPGSQVNLSALRFRFRFRALKATSVISGLKIVIGAL 243
Db 185 aftfirdpwnwldfsvliamayttefv-dlgnvsalrfrvrlralktisvsglktivgal 243
Qy 244 LRSVKVLVDVWMLTFLCLISIFALVQQLFMGLINQKCIKHNCGNPNA----- 290
Db 244 lqsvkkladvmvltvfcslvsfaliqlfmgnlrhkvrnftalngtngsveadglvves 303
Qy 291 -----SNKDCFEKEKDEDFIMCQTWLGSRPCPNGSTCDKTTLPNDNNYTKDFNFGWSFL 345
Db 304 ldlylsdpenyilkngtsdvllcngssdagtcpegycclkgapndhgytfsdfawaf1 363
Qy 346 AMFRVMTQDSWERLYRQILRTSGIYFVFFVFWVFLSGFYLLNLTAVVTWAYEEQNRNV 405
Db 364 alfrimtgdcwerlyrqtlrsagkiymifmlviflgsfylnlilavvamayeegnat 423
Qy 406 AAETEAKEMFOEAQQLLREEKEALVAMIDRSSLSNLSQASSFSF-----KKRRPFG 457
Db 424 iaeteekkrfqaemmlkhealtirgvdtsrslslemaplavpnsherrkirkms 483
Qy 458 S-----KTRKS-----KTRKS-----FFMRGSKTAQASA 476
Db 484 sgteecgedrlpksdsedgpramnhlsitrgltsmtmkprsrsgsiffrldlgseadf 543
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Qy	477	DSDEDAASKN-----POLLBOQTKRLSONLP-----	501
Db	544	addenstareshtsllvplwprlrtsaaqgspgtsapghalhghkknstvcngvvs1	603
Qy	502	-----VDLFDEHVDPLHRQ	515
Db	604	lgaqdpeatspgshllrprvmlhepddttptseepggpqltsqapcvdgtlee---pgarq	660
Qy	516	RALSAYSILRITIOEQEKPEPCFCGKNLASKYLVWDCSPQWLCIKKVLRTINTDPFTE	575
Db	661	raisaavalsaleesrhkcpcpwnraqryliwecclwmsikqgvklvmdpftd	720
Qy	576	LATICIIINTVFLAVEHNMDDNLKTILKIGNVFTGIFTAEMCLKIIALDPHYHFRHG	635
Db	721	ltitumcivlnltlmalchymmsefeemlqgnlvftgftaentfklialdpyvyfqqg	780
Qy	636	WNVPFDSIVALLSDADVLYNTLSDNNRSFLASURVLURFKLAKSWPTLNTIKIIGHSVGA	695
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Qy	696	LGNIITVVLTVIVFISVGMRLFGTKFNKATAYATQERPRRRWHDNFYSHFLVVRILCG	755
Db	839	lgnltvlalvifavgmqlfgknyselr-dsdsgilprwhmddfhaflilrilcg	897
Qy	756	EWIENMWGCMQDMSGPLCIIIVFLIWIYIGKVLVNLFIALLLNSFSNEKDSLEGETR	815
Db	898	ewietmwdcm-evsgsgslclvlflvmvignlvlnflialllssadnltapde-dre	955
Qy	816	KTKVQALDRFRRAFFMLHALQSFCKKCRK-----NSPKPKE	855
Db	956	mmnlqlalariqlrglrvtrttwdfccglrlhrpqkpaalaaqqglpsciatpyspppde	1015
Qy	856	TTSESFAGENKDSLDPARPWKYEDTMALYTCQAGAP---LAPLAEVEDDV--EYCGEGG	910
Db	1016	tek-----vpbtrketgeegpggtpgdppevcvpiavesdtddqeedeen	1065
Qy	911	ALPTSOHSAGVQAGDL-----PPETK--OLTSPDDQGVEMEVFSEEDLH----LSIQ	956
Db	1066	slgteesshkqgesqpsvgwprgpdpdrctwsqvsatasaeaea--sqadwrgqwkaeqp	1124
Qy	957	SPRKKSDAVSMLSECTSIDLN---DIFRMLQKTVPKQPDRCPFKGLSCHFLCHTKDKR	1013
Db	1125	apgcgetpedscesgstadmtntaelleqpdlgdgvkdpedctfegcrrpcpccavdtt	1184
Qy	1014	KSPWLLMWNTRKCYOIVKHSVPESFIPIVILLSSGALIFEDYNLPSRPQVEKLLRCTDN	1073
Db	1185	qapgvwvrlrktcyhlvshwvftetfifmlllsgalafediyleerktikvlileyadk	1244
Qy	1074	IFTFIFLLEMLKAWAFGRFRVFTSACWLDPLIVVSVLSIM-----NLPSLSKSFRT	1126
Db	1245	mftyvrvlemlkwaaygfkkyftnacwclfdlvvdsivslvantlfgfaempikslrt	1304
Qy	1127	LRLRPLRALSQFEGMKVYVYALISAIPAILMVLVLCLIFWLVCILIGVNLFSKGFGRCI	1186
Db	1305	lralrplrasrfegmrvvvnalvgaipsmvlvclifwlifsmgvlfnagkfgrci	1364
Qy	1187	NGTDINMYLDFTVPNRSOGCNSINYS----WKVPOVNFEDNVGNAYLALLQVATYKGMLEI	1242
Db	1365	nqtegdplnytlvnnksqceslnltgeltywtkvknfdnvvgaylallgvatfkvmvdi	1424
Qy	1243	MNAAVDSREKDEOPDEANLYALVYVVFPIFGSFETLNLFGVITINFNOOKKLGQOD	1302
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Qy	1303	IFMTTEOKKYNNAMKLGTKPKQKPIPRPLNKCQAFVFDLTVSQVDFVITLGLITVLNMII	1362
Db	1485	ifmteeqkkyynnammklsgskpqkpiprplnkyygfifdvtkqafdvimfliclnmvt	1544
Qy	1363	MMAESADQPKDVKKTTDIINIAFVIFTTECLIKVFAURQHYFTNGWNLFDVCVVVUSII	1422
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2002, 22:39:50 ; Search time 61.5 Seconds
(without alignments)
645.826 Million cell updates/sec

Title: US-09-646-224A-2

Perfect score: 9173

Sequence: 1 MEERYPVIFPDNRFRPTVFCNGDLSSLDVAKVKVHND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4669.5	50.9	1956	4	US-08-843-417-10
2	4562	49.7	1969	3	US-08-836-325-16
3	4541.5	49.5	1984	3	US-08-836-325-10
4	4508.5	49.1	1989	3	US-08-836-325-12
5	4506	49.1	1956	4	US-08-843-417-2
6	4479.5	48.8	2005	3	US-08-836-325-7
7	4394.5	47.9	1978	3	US-09-024-020B-3
8	4390.5	47.9	1988	3	US-09-024-020B-4
9	4388.5	47.8	1989	3	US-08-836-325-11
10	4316.5	47.1	1976	3	US-09-024-020B-9
11	4185	45.6	1835	3	US-08-836-325-15
12	3554.5	38.7	2105	2	US-08-808-793-3
13	3554.5	38.7	2105	3	US-08-772-512A-3
14	3550.5	38.7	2104	2	US-08-808-793-4
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16	3532	38.5	2100	2	US-08-808-793-23
17	3532	38.5	2100	3	US-08-772-512A-19
18	3242.5	35.3	1820	3	US-07-998-289B-8
19	2593	28.3	1011	3	US-08-836-325-2
20	2085.5	22.7	813	3	US-08-836-325-8
21	1505	16.4	1872	6	5386025-6
22	1497.5	16.3	1873	1	US-08-435-675B-4
23	1488	16.2	2161	1	US-08-455-543A-51
24	1488	16.2	2161	2	US-08-223-305C-45
25	1487.5	16.2	1873	1	US-08-336-257A-7
26	1480	16.1	2161	1	US-07-745-206A-2
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31	1468.5	16.0	1968	2	US-08-223-305C-45
32	1443	15.7	2516	3	US-08-374-077C-2
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40	1410	15.4	2337	3	US-08-713-118-2
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44	1306	14.2	452	3	US-07-998-289B-6
45	1187	12.9	413	2	US-08-808-793-25

ALIGNMENTS

RESULT 1
US-08-843-417-10
Sequence 10, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-843-417-10

Query Match 50.9%; Score 4669.5; DB 4; Length 1956;
Best Local Similarity 51.1%; Pred. No. 0;

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-16

Query Match 49.78; Score 4562; DB 3; Length 1969;
Best Local Similarity 49.98; Pred. No. 0;
Matches 961; Conservative 281; Mismatches 454; Indels 230; Gaps 34;

Qy 11 PDENFRPFTSDSLAAIKRIAIOKERK-KSKDAAABPQPPOLDLKASRLKPLKYGDI 69
Db 7 PGOSFVHTKQSLALTEQRAERKSKPEKEKDDDEAPKPSDLEAGKQLFFIYDI 66
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Db 127 LFSLMILCTILNCFMNNPPDWTKNV-GYTFGTGIFTFESLKLARGFCVGEFTLR 185
Qy 190 DPWNWLFIVGTATATCFPGSQVNLASALRTRFRVFRALKATISVGLKVIIVGALLRSVKK 249
Db 186 DPWNWLFVIVFAYLTFEV-ILGNVSALRTRFRVLRALKTISVPLGLKTIIVGALLIOSVKK 244
Qy 250 LVDVWVLTFLCSIFALVQOGLFMGLNKGKICIKHNCGNPNA--SNKDCFEKEK----- 301
Db 245 LSDVMILTFLCSVFLALIGLQFMGLNKGKICFRNSLENNETLESIMNTLESEEDFRKYFY 304
Qy 302 ----SEDFIMCGTWLGRPCNGSTCDKTTLNPNNTYKFNFGWSFLAMFRVMTQDSWE 357
Db 305 YLEGSKDALLCGFTSDSGCPEGTCVKIGRNPDPYGYTSTFTSWAFLALRLMTQDYWE 364
Qy 358 RLYQOILRTSGIYVFFVFFVIFLGSFYLLNLTAVVTMAYEEQNRNVAAEAKKFKQ 417
Db 365 NLYOQTLRAAGKTYTFFVFFVIFLGSFYLLNLTAVVTMAYEEQNRNVAAEAKKFKQ 424

Qy 418 EAQQLLR--BEKEALVA-----MGIDRRSLNSLQASSFPKRRKFKGSK-- 459
Db 425 QMLDLRKKQEAEAAIAAAAEYTSIRRSIRIMGLSESSSETSKLSSKAKERRNRKKN 484
Qy 460 -----TRKSPFM----- 466
Db 485 QKLLSSGEEKGDAEKLKSKSESDSIRRSKSFHLGVGHRRAHEKRLSTPNQSPLSIRGSLF 544
Qy 467 ---RGSKT-----AQSASDSE-----DDASKNPQL-----LEQ 492
Db 545 SARSSRTSLSFKGRGRDXGETEFADDEHSIFGDNESRRGSLFVPHRPXERRSNISQ 604
Qy 493 TKRLSQNLQVDP-----LF 505
Db 605 ASRSPMLPVNGKMHSAVDCNGVSLVDGXSAALMPLNGOLLPEGTNTQIHKKRRCSYLL 664
Qy 506 DEHV--DPLHRQALSAVSILTIIOEQEKFOEPFCPCGNKLASKYLWDCSPQWLCKKK 563
Db 665 SEDMLNDPNLRQRAMSRASILTNTVEELESQKCPMPWYRFAHKLFIWNCSPYIKFKK 724
Qy 564 VLRTIMTDPFTELAITICIIINTVFLAVEHHNMDONLTKILKIGNWVFTGIFIAEMCLKI 623
Db 725 CIYFIVMDPFVDLATICIVLNTLPMAHEHPMTTEFNVLGAIGNLVFTGIFPAAEMVKL 784
Qy 624 IALDPYHYFRHGNVDFDSIVALLSLADLYNTLSD--NRSFSLASLRLRVFKLAKSWPTL 682
Db 785 IAMDPEYFQVGNIFDSLIIVTSLVELF---LADVEGLSVLSRFLRLRVFKLAKSWPTL 841
Qy 683 NTLKIIICHSVGALGNLTIVLTIIVFISVGVMRFLFGTKFNK-TAYATQERPRRRHMDN 741
Db 842 NMLKIIIGNSVGALGNLTIVLTIIVFISVGVMRFLFGTKFNK-TAYATQERPRRRHMDN 901
Qy 742 FVHSLVVFIRILCGEWMNMGDMODGSPLCIIVFVIMVIGLVNLFIALNLASF 801
Db 902 FFHSLIVFVRLCGEWMNMGDMODGSPLCIIVFVIMVIGLVNLFIALNLASF 960
Qy 802 SNEEKDGSLEGETRKTQVQLADLDRFRRAFSPMLHALQSCCKKRRKNSPKKTESFA 861
Db 961 SSDNLT-AIEEDPDANNLQIAVTRIKKGINVYKQTLREFILKAF---SKKPKISREIQ 1015
Qy 862 GENKDSILPDAPPKE-YDTDMALYTGAGAPLAPLAIVEDDVEYCGEGGALPTQSHSG 920
Db 1016 AE-----DLNTKKENYISNMTLAEMSKG---HNFLKEKDKISGSSXDKHLMEDSDG 1065
Qy 921 VOAGDLPETKQL-TSPDDQGVEM--EYFSEEDLHLSIQSPRKSDAVSMLESCSTFDLN 977
Db 1066 QSFTHNPSTVTVPIAPGESLDMNEELSSDSD---SYSKNRSS-----SECTVDNP 1116
Qy 978 DIFRNLOKTVSPKQDRCFPKGLSCHFLCHTKDRKSPWLMWNIRKTCYQIVKHSWF 1037
Db 1117 LPGEGEAEAPNDPEACFTDGCVRREFSCQOVNIESGKGIWNNIRKTCYKIVHSWF 1176
Qy 1038 SFILFVILLSSGALIFEDVNLPSRQVEKLLRCTNITFFLEMLKWKVAFGRPRFT 1097
Db 1177 SFIVMLILLSSGALAFEDIYIERKTKIILEYADKIFTYFIFLEMLLKIAWYGYKTYFT 1236
Qy 1098 SAWCWLDLIVVYVLSLM-----NLPSLKSFTLRLALRPLRALSOFEGMKVYVYALI 1150
Db 1237 NAWCWLDLIVVYVLSLM-----NLPSLKSFTLRLALRPLRALSOFEGMKVYVYALI 1296
Qy 1151 SAIPAILNVLVCLIFLWVLCILGNLPSRQVEKLLRCTNITFFLEMLKWKVAFGRPRFT 1206
Db 1297 GAIPSIMVLLVCLIFLWVLCILGNLPSRQVEKLLRCTNITFFLEMLKWKVAFGRPRFT 1355
Qy 1207 NIS-NYSKVKVQVNDVGNAYLALLQVATYKGLWEIENNAVDSREKDEQDPDFEANLYAY 1265
Db 1356 NVSQNRWKNLKVNDVGNAYLALLQVATYKGLWEIENNAVDSREKDEQDPDFEANLYAY 1415
Qy 1266 LVYVFFIIFGSEFTLNLFIGVIIDNFNOOKKLGQDIFMTTEQKKYNNAMKLCGTCKPO 1325
Db 1416 IYVFFVFIIFGSEFTLNLFIGVIIDNFNOOKKLGQDIFMTTEQKKYNNAMKLCGTCKPO 1475
Qy 1326 KPIPRLNKCQAFVFDLVTQVDFVILGLIVLNMIIIMAESADQPKDKVKTFTDILNTAF 1385

Db 1476 KPIPRGNKIOGCFDLVTNOAFDISIMVLICLANNVTMVEKEGOSQHMTEVLYMINVF 1535
Qy 1386 VVITIECLIKVAFALROHYFTNGNLEPCVVVLSIISTIVSRLESDISFPPTLFRVVR 1445
Db 1536 IILFTGECVLKLSLRHYFTVGNIPDFVVVLSIISVGMFLADLIET-YFVSPILFRVIR 1594
Qy 1446 LARIGRILRVRAARGIRTLFALMMSLPSLFNIGLLFLVWFYIAIFGMSWFSKVKRGS 1505
Db 1595 LARIGRILRVKAGKIRTLFALMMSLPALFNIGLLFLVWFYIAIFGMSWFSKVKRGS 1654
Qy 1506 GIDIFNPETFGMLCULFQITTSAGNDTLNPMLEAKE-----HCNSSQDSOQOP 1557
Db 1655 GINDMFNETFGNSMCLFQITTSAGNDGLLAPILNSKPPDCPKKVPKHPGSSVEGDCGNP 1714
Qy 1558 QIAVYFVSYIIISFLVWVNYIAVILENFNTATEESDPLGEDDFEFYEVWEKFDPEA 1617
Db 1715 SVGIFYFVSYIIISFLVWVNYIAVILENFNTATEESDPLGEDDFEFYEVWEKFDPEA 1774
Qy 1618 SQFIQSALSDFADALPEPLRVAKPNKFOFLVMDLPMVMGDRLCMDVLFATFTRVLGDS 1677
Db 1775 TQFIEFKLSDFAAALDPLLIAPKNKQVLIAMDLPVMSGDRHCLDILFATFTRVLGES 1834
Qy 1678 SGLDTKMTMEEKFMENPFKKLYPIVTTTKRKEEGQAAVIOQRAYRKHMEKMKVLRK 1737
Db 1835 GEMDSLRQMEERFMSANPSKVSVEPIITTLKRKQXVSATVIOQRAYRY-----RLRQN 1889
Qy 1738 DRSSSS 1743
Db 1890 VKNISS 1895

RESULT 3

US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halebouga, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203.
REFERENCE/DOCKET NUMBER: 0917.02400002.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-10

Query Match 49.5%; Score 4541.5; DB 3; Length 1984;
Best Local Similarity 48.9%; Pred. No. 0;
Matches 954; Conservative 291; Mismatches 443; Indels 263; Gaps 35;
Qy 11 PDERNFRPFTSDSLAAIKKRIATQKQK-KSKDKAAAEPPQRPQLDLKASRKLPLKYGDI 69
Db 7 PGQSFVHTTQSLALIEORISEEKAKHEKDEKDEEGPKPSSDLEAGKQLPFIYDI 66
Qy 70 PPELVTRPDLDPYKDKHTFMVNLKRTIYRSASRALFILGPNFLRSLRIMIRISVHS 129
Db 67 PPGMVSEPLEDLPYADKTFIVLNKCKAIFRENATPALYMLSPSPLRISIKILVHS 126
Qy 130 VFSMFICTVIINCMFMANSMERSFDNDIPEYVFTGIIVLEAVIKILARGFIVDEFSLR 189
Db 127 LFSMLIMCTILTNCFMTLSNPPEWTKNV-EYTFGTIYTFESLIKILARGEVCGVFTFLR 185
Qy 190 DPWNWLDPIVIGTATATCFPGSQVNLSALRTFRVFRALKAISVLSGLVIVGALLRSVKK 249
Db 186 DPWNWLDPIVIVAYLTFEV-NLGNVSALRTFRVLRALKTSIVPLGKTIYVGLIYQSVKK 244
Qy 250 LVDVNVLTFLCLSFALVGOOLFMIKQKCIKHNKGNPA--SNKDCFEKED----- 301
Db 245 LSDVMILTVCLSVFALIGLQFMGNLKHCKFRKELENETLESIMTAESEELKKYFY 304
Qy 302 ----SEDFIMCGTWLGRPCNGSTCDKTTLPDNNYTKFDFNGWSFLAMFRVMTQDSWE 357
Db 305 YLEGSKDALLCGFTSDSQCPGEGYICVAGRNPDYGTSTFTSWAFALFLMTQDYWE 364
Qy 358 RLYQILRTSGTYFFVFFVFFVFLGSLFYLLNLTAUVIMAYEQNNRNVAAETAEKQWFO 417
Db 365 NLYQOTLRAAKTYMIFVFFVFFVFLGSLFYLLNLTAUVIMAYEQNNRNVAAETAEKQWFO 424
Qy 418 EAQOLLR---BEKEALVA-----MGIDRSSLSLQASSFSFPPKRR----- 453
Db 425 QMLDRLKKEQEEAIAAAAAAEFTSIGRSRIMGLSESSSETSRLLSSKSAKERRNRKKKK 484
Qy 454 ----- 453
Db 485 QKMSGEEKGDDEKLSKSGSEESIRKKSFHILGVEGHHTREKRLSTPNQSPLSIRGSLFS 544
Qy 454 -----KFFGSKT-----RKSEFM-----RGSKTAQA 474
Db 545 ARRSRTSLFSFKGRDLGSETEFADDEHSIFGDNESRRGSLFVPHPRRRSSNISQA 604
Qy 475 SASD-----SEDDASKNPOLL 490
Db 605 SRSPVLPVNGKMHSAVDCNGVSLVDGPSALMLPNGQLPEVIIDKATSDSGTTNQ- 663
Qy 491 EQTKRLSON--LPVDLDFEHVDPLHRQALSAVSLITITIOEQEFQPCPCGNKASK 548
Db 664 -RKRLSSSYFLSEDMLN---DPLHRQAMSRASILTNTVEELESROKCPWYRFYHT 719
Qy 549 YLVWDCSPQWLCIKKVLRTIMTDPTELAITICIIINVLAVEHHNMDNLKTLIKCN 608
Db 720 FLIWNCSFYWIKFKKLIYFIVWDFVDLAITICIVLNTLFNAMEHHPTEFEKNVAVGN 779
Qy 609 WFTGIFTAEMCLKIIALDPYHYFRHGNVFDISVALLSLADLYNTLUSD--NNRSFLASL 667
Db 780 LIFTGIFAAEMVLKLIAMDPEYFQVGNIPFDSLIVTSLTLELF---LADVEGLSVLRSF 836

QY 130 VFSMFIICVTIINCMFMANSERSFDNDIPYVFIIGVILEAVIKILARGFIVDFFSFLR 189
Db 127 LFSLMINTILTCIFMISNPPETKNV-CYTFGTIYTESLIKILARGCEFTFLR 185
QY 190 DPNWNLDFIVIGTAIATCFPGSQVNLGALRTFRVRALKALISVTSGLKVIIVGALLRSVKK 249
Db 186 DPNWNLDFIVFAYLAFEFV- NLGNVSALRTFRVLRALKTISVIPGLKTIIVGALIQSVKK 244
QY 250 LVDVMTLTLCLSTFALVGOOLFMGILNOKCIKHNCGNPNA--SNKDCFKEKD----- 301
Db 245 LSDVMILITFCLLSFVAGILQGLFMGNLKHCKFRKELENETLESIMNTAESEELKYFY 304
QY 302 ----SEDFIMCGTWLGRPCNGSTCDKTLNPNNTTKFDFGWSFLAMPFRVMTQDSWE 357
Db 305 YLESGKALLCGFTSDSQCEGIVCVKAGRPDYGTISDTFSWAFALFRMTQDIWE 364
QY 358 RLYQOILRTSIYVFFVFFVIFGSLYLLNLTLAVVTMAYEONRNVAATEAKERMFQ 417
Db 365 NLYOQTLRAAGKTYMIFVFFVIFLGSFYLLNLILAVVAMAYEQNANIEAKOLEFEQ 424
QY 418 EAQOLLR---EKEALVA-----MGIDRSLNSLOASSPSPKKR----- 453
Db 425 QMLDLRAKEQEAIAAAAAAFTSIRRSIRIMGLSESSESSETSRUSSAKERRNRKKK 484
QY 454 ----- 453
Db 485 QKXSSGEEKGDEKLSKSGSEESIRKSPHILGVEGHHRTREKRLSTPNOSPLIRGSLP 544
QY 454 -----KFTGSKT-----RKSPFM-----RGSRTAQ 473
Db 545 SARSSRTSLFSFKGRGRDLGSETAFADDEHSIFGDNESRRGSLFVPHRRPRSSNISQ 604
QY 474 ASASD-----KDGSAKPNOL 489
Db 605 ASRSPVLPVNGKMHSAVDCNGVVSVDGFSALMLPNQOLLPEVIIDKATSDSGTNNOM 664
QY 490 LEQTKRLSON--LPVOLDDEHVDPLHRQALSAVSILITITIQOEKQPECFPCGKNLAS 547
Db 665 --RKRLSSSYFLSEDMLN--DPLRQRAMSRASILTNTVEELESQRKCHQLLYRFAX 719
QY 548 KYLVWDCSPQWLCKKVLRTIMTDPFTTELATITICIIINTVFLAVEHNMNDNLTKILIG 607
Db 720 TFLWNCSPWIKFKLITYFIVMDPFVDLAIITICIVLNTLFMAHEHPMTPEEFKNVLAVG 779
QY 608 NWVFTGFIEMCKLIADLPYHFRGWNVDGSIVALLSLADLYNTLSD--NRRSFLAS 666
Db 780 NLIFTGFAEMVLKLLAMPDEYFQVGNIFDSLIVTSLIELF---LADVEGLSVRS 836
QY 667 LRVLRFKLSKSWPTNLTKIIGHSVGALGNLTIVVIFSVGMRLFGTKFNK-T 725
Db 837 FRLLRVEKLAKSWPTNLTKIIGNSVGLGNLTIVLAIIVFPAVVGMLFGKSYKECV 896
QY 726 AYATOERPRRWMDNEHSHFLVFRILCGEWIENMGCMQMDGSPLCIIVFVLIWVIG 785
Db 897 CKINVDCKLRWMDNEHSHFLVFRILCGEWIETMDWCM-EVAGQTMCLIVVMVWVIG 955
QY 786 KLVVNLFIALLNSFNEKDGSLGCTRTKTVQLALDRFRFRAFSMLHALQSFCKKC 845
Db 956 NLVVNLFLALLSSFSDDNLT-AIEEDTDANNLQIAVARIKRGINVKOTLREFILKSF 1014
QY 846 RRKNSPKPKETTESFAGEN--KOSILDPARPKWEYDTDMALYTGQAGAPLAPAEVEDV 903
Db 1015 SKK--PKGSKDTRTADPNKNKNYISN-----RTLAEMSKDH 1050
QY 904 EY-----CGEGALPTSQHSAGVQAGDLPPETKQLTSPDDQG-VEVEVFSEEDLHLSI 955
Db 1051 NFLKEKDRISGYSGLDKSPWENDYQSFTHNPSTVTVPIAPGESLEIMNTTEELSSDS 1110
QY 956 QSP--RKKSADVAMLSSECTID--LNDIFRNLQKTVSPKQPDRCFPKGLSCHFLCHTKD 1012
Db 1111 DSDYSKEKRNRSSSECTVDNPLPGEXEAEAEFPVNADEACFTDGCVRFPCCQVNV 1170
QY 1013 RKSPWLVWNRIRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVNLSPRQVEKLLRCTD 1072

Db 1171 DSGKGVMTIRKTCYRIVBHSWFESFIVLMLSSGALAFEDIVIEKKTKIILEYAD 1230
QY 1073 NIFTFIFLLEMLKWAFFRFRYTSACWKLDFLIVVSVLSLM-----NLPSLKSF 1125
Db 1231 KIFTYIFILEMLLKWAYGYKTYFTNACWKLDFLIVDVSFLTAVANTLGYSDLGPISLR 1290
QY 1126 TLRALRPLRALSQEGKVVVYALISAPAILNVLNVLCLIFELWVFCILGVNLSGKFGRC 1185
Db 1291 TLRALRPLRALSREGMVVMVVALIGALPSIMNVLNVLCLIFELWVFCILGVNLSGKFGRC 1350
QY 1186 INGTDINMYLDFTEVPNRSQC-----NIS--NYSWKVPQVNFNDVNGVAYLALQVARYKGL 1240
Db 1351 VNTDGSRF-PTSQVANNRSECFALMNVSGVNRWNLKVNFDVNGVGLYLSLQVATFKGM 1409
QY 1241 EIMNAVDSREKDEQDPFEANLYAYLVFVFIIFGSFETLNLFGIIVIDNFNOQKKLGG 1300
Db 1410 DIMYAAVDSVNVNEQPKYEYSLYMYIVFVFIIFGSFETLNLFGIIVIDNFNOQKKLGG 1469
QY 1301 QDIFMTBEOKKYNNAMKLGTKPKQKIPRPLNKQAFVFDLVTISOVDVILGLVLNM 1360
Db 1470 QDIFMTBEOKKYNNAMKLGSKPKQKIPRPGNKFPQGCIFDLVTNQAFDITIMVLCUNM 1529
QY 1361 IIMMAESADQPKVKKTFDILNIAFVWIFTTECLIKVFPALRQHYFTNGWNLFDQVWVLS 1420
Db 1530 VTMVVEKEGOTEYMDYVYLHWINMVFIILFTGCEVLKLSLRHYFTVGVWNLIFYVWVLS 1589
QY 1421 IIST-LVSRLEDSISPPPTLFRVVRVLARIGRILRLVRAARGIRTLFALMMSLPSENI 1479
Db 1590 IVGMFLAEMIEKYEVS--PTLFRVIRLARIGRILRLKAKGIRTLFALMMSLPALFNI 1647
QY 1480 GLLLFLVWFYIAYFGMSWFSKVGSGIDDLNFETETGSMCLCFQITTSAGWDGLLAPI 1539
Db 1648 GLLLFLVWFYIAYFGMSNFAIVYKKEAGINDMFNETFGNSMCLCFQITTSAGWDGLLAPI 1707
QY 1540 LEA-----KEHCNSSQSCQPOQAVVYFVSYIISLIVVNMVIAVILENFAT 1591
Db 1708 LNSAPPDCPKKVPHGSSVEGDCGNPSVGIFYFVSYIISLIVVNMVIAVILENFAT 1767
QY 1592 BESEDPGEDDFEYFVWEKFDPEASOFIOYALSDFADALPEPLRVAKPNKQFLVMD 1651
Db 1768 BESEDPGEDDFEYFVWEKFDPEASOFIOYALSDFADALPEPLRVAKPNKQFLVMD 1827
QY 1652 LPVMYGRDLCHMDVLAFTVRLVGLSGSLDTMKTMMKEKFMENPFKLYPIVTTTKRK 1711
Db 1828 LPVMYGRDLCHMDVLAFTVRLVGLSGSLDTMKTMMKEKFMENPFKLYPIVTTTKRK 1771
QY 1712 BEEQGAIVQIARRK-----HMEKMKVLRKLD 1738
Db 1888 QEEVSATIIQIARRYRLRQHVKNKNISSYIKD 1919

RESULT 5
us-08-843-417-2
; Sequence 2, Application us/08843417
; Patent No. 6184349
; GENERAL INFORMATION:
; APPLICANT: Herman, Ronald C
; APPLICANT: Deigado, Stephen G
; APPLICANT: Fish, Linda M
; APPLICANT: Sangameswaran, Lakshmi
; APPLICANT: Rabert, Douglas K
; TITLE OF INVENTION: CLONED PERIPHERAL NERVE
; TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: Heller Ehrman White & McAuliffe
; ADDRESS: 525 University Ave
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94301
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843.417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: dorsal root ganglia
CELL TYPE: peripheral nerve
US-08-843-417-2

Query Match 49.1%; Score 4506; DB 4; Length 1956;
Best Local Similarity 50.7%; Pred. No. 0;
Matches 962; Conservative 269; Mismatches 443; Indels 222; Gaps 38;

Qy 15 NFRFTSDSLAAKRIAIQERKSKDKAAAE-----PQRPQLDLKASRLPKLYGDP 70
Db 12 NFRFTPSLAEIEKQIAAHAARKARTKRGQEDKGKPRQLDLKACNLKPYFGELP 71

Qy 71 PELVTKPLEDDPYKDKHTFWLNKRTIVRFSAKRALFLILGPNLRSIMIRISVHSV 130
Db 72 AELVGELEDLPYVTHRTFWLNKRTISRSATWALWLFSPNLRTTAIKSVSHV 131

Qy 131 FSMFTICVIVNCMFMANSERSFNDIP---EYVFIGIYLEAVIKILARGFIVDEPSF 187
Db 132 FSIPTITILVNCMTRT-----DLPEKVEYVFTVYITFEALIKILARGFCLNEPTY 184

Qy 188 LRDPMNLDFIVIGTAICTPGSOVNL---SALRTFRVFRALKAISVISGLKVIIVGALL 244
Db 185 LRDPMNLDFSVITLA-----YVGAIDLRGISGLTRFRVLRALKTVSVIPGLKVIIVGALI 240

Qy 245 RSVKRLVDVMTLFLCLSFALVGQOLPMGILNOKIKHNGCPNPASNKDCFEK----- 299
Db 241 HSVKRLADVTILTVFCLSVFALVGLQLFKGNLKNKICIRNGTDPHKADNLSEMAEYIFIK 300

Qy 300 KDSDFIMCGTWLGRPCNGSTCDKTLNPDNNYTKFDNFCWSFLAMFRVMTQDSWRL 359
Db 301 PGTTDPLLCGNSDAGHCPGVVCLKTPDNPDFNTSETSDSAWFLSLFRLMTQDSWRL 360

Qy 360 YRQILRTSGIVFVFFVVFVIFLGSFYLNILAVVVMAYEQBNRVAETAERKMFQEA 419
Db 361 YQOTLRASGKMYVFFVIFLGSFYLVNLIILAVVVMAYEQSOATAEIEAKEKFFQEA 420

Qy 420 QOLLREEKALVAMGIDRSSNLNSLQASSFSP-----KKRKFSGS----- 458
Db 421 LEVLOKEVJLAALGIDITLSQSHSGSLASKNANERRPRKRSVSEGSTDDNRSPOSDP 480

Qy 459 ---KTRKSPFMRSKTAQAS-----ASDSED----- 481
Db 481 YNORMSFLGLSGRRRASHGVFHRAPSQDISPPDGITDDGVPHGDOESPRGSIILGR 540

Qy 482 -----DASKNP-----OLLEQTKRLSNLNP-----VDLDEHV----- 509
Db 541 GAGQTGPLRSPPLQSPNPGRRHGEGLGVPTGELTAGAPEGPALDTTGOKSFLSAGYL 600

510 -DPLHRQALSAVSILITITIQEQRFBQPCPCGKNLASKYLWDCSPQWLCIKKVLRTI 568
Db 601 NEPPRAQAMSVSVSMTSVIEELEBSKLKPCCLISFAQKYLWECCKPKRKFKNALFEL 660

Qy 569 MTDPTLAIYICIIINTVFLAVEHHNMDNLKTTILKIGNVFTTGIFTAEMCLIKIILDP 628
Db 661 VTDPEALTITLCIIVNTVFMAHEHYPTMDAFDALQAGNIVFTVFTTMEAFKIAIEDP 720

Qy 629 YHPRHGNVFDSTIVALLSLADVLNLTSDNNRSFASLRLVRVFKLAKSWPTLNTLKI 688
Db 721 YYYFQKKWNIIFDCVIVTVLSLEL--SASKKGLSVLRTFRLRLVRVFKLAKSWPTLNTLKI 778

Qy 689 IGHSVGA LGNLTIVLTVIVFVSVVGMRLFGTKF--NKTATATQERPRRRHMDRYHSF 746
Db 779 IGNSVGA LGNLTIFILAIIVFIFALVGKQLLSEDDYCKRGDGVSVWNGEKLWMCDFHSHF 838

Qy 747 LVVFRILGWIENWGMCMQMDGSPICITIVFLVIMVIGLVNLTALLNSFSNE-- 804
Db 839 LVVFRILGWIENWVCM--EVSQKSIICILFLTVWVGLNVLVNLFTALLNSFSADNL 897

Qy 805 ---EKDGSLEGETRKTQVQLALDRFRRAFSFMLHALQSCCKCKRKNKSPKPKETE--- 858
Db 898 TAPEDDGEV-----NLIQLALARIQVILGHRASRAIASYISSHCRPR---WPKVETQLGM 948

Qy 859 ---SPAGENKDSILPDA-----RP-----WKKEYDTDMALYTCQACAPLA--- 894
Db 949 KPPLTSSEAKNHIATDAVSAAGVNLTKPALSFPKENGHGDFTIDPNVW---VSVPTAEGES 1005

Qy 895 PLAEVEDDVEYC-----GEGALPTSQHSAGVOAGDLPPETKOLTSPDDQGVEM 943
Db 1006 DLDELEDEMEQASQSSWQEDPKGOEQLPQVKQENHQAARSP--ASMMSSEDLAPYLG 1063

Qy 944 EVFSEDLHLSTQSPRKSDAVSMLESECTIDLND---IFRNLQKTSVPKPDRCFPKG 1000
Db 1064 ESWKRKD---SPQVPAEGVDDTSS--SEGSTVDCPOPEELRKIPELADLDEPDCFTG 1119

Qy 1001 LSCHFLCHKTDRKSPVLMWNIRKTCYQIVKHSFESFIIFVILLSSGALIFDVNLPS 1060
Db 1120 CTRRCPCCNVNTSKSPWATGQVKTCTYIVHSFESFIIFMILLSSGALAFEDNLEE 1179

Qy 1061 RPQVEKLLRCTDNITFFILLEMILKVAFGPRRYFTSAWCWDLFIVVSVLSLM--- 1116
Db 1180 KPRVKSLEYTRDVTFTFVFEMLLKWAYGFKYFTNAWCWDLFIVNLSLTIKTL 1239

Qy 1117 ---NLPSLKSFTLRALRALSQFEGKVVVYALISAIPAILNVLVLLFVLCIL 1173
Db 1240 EYSDVASIKALTRLRALRALSREFGMRVVDVLAIPAISIMNVLVLLFVLFISLM 1299

Qy 1174 GVNLFSGKFGRCINGTDINMY--LDFTVPPNRSOCNISN---YSWKVPOVNVFNVGNAY 1227
Db 1300 GVNLFAGKFSKVD--TRNPPFSNVNNTWVNNKSECHNQSTGHFFWVNVKVN-----Y 1351

Qy 1228 LALLQVATYKGLWEIMNAAVDSREKDEQDFEALNYAYLYFY-----VFIFGSFFTL 1280
Db 1352 LALLQVATFKGMDIMYAAVDSGEINSQPNWNNLYVLYFVFDVNVAMGVFIIFGFFTL 1411

Qy 1281 NLFIGIIVDINFNOQKGLGGQIDFMTBQKYYINAMKLGTKKPKOKPIPRPLNKQCAFVF 1340
Db 1412 NLFIGIIVDINFNOQKGLGGQIDFMTBQKYYINAMKLGSKKPKOKPIPRPLNKYQGVVF 1471

Qy 1341 DLVTSQVDFVILGLIIVLNMIIMMAESADQPKDVKTDFILNIAFVIFTIECLIKVPA 1400
Db 1472 DLVTSQVDFVILGLIIVLNMIIMMAESADQPKDVKTDFILNIAFVIFTIECLIKVPA 1531

Qy 1401 RQHYETNGNLPDCVVVVLSTIISLVSIR--LEDSDISFPPTLFRVRLARIGRILVRAA 1459
Db 1532 RQHYETNGNLPDCVVVVLSTIISLVSIR--LEDSDISFPPTLFRVRLARIGRILVRAA 1591

Qy 1460 RGIRTLFALMMSLSFLNIGLILFLVMPFIYAFGMSWFSKVKSGIDDIINFETFGS 1519
Db 1592 KGIRTLFALMMSLSFLNIGLILFLVMPFIYAFGMSWFSKVKSGIDDIINFETFGS 1651

Qy 1520 MCLCFQITTSAGWDTLLNPMLE-AKEHC-----NSSQDSQOQIAVAVVFSVILISF 1572
Db 1652 MCLCFQITTSAGWGLSPILNPPYCDPLNPNNSGRGCGSPAVGIIFFTHYIISF 1711
Qy 1573 LIVNMYIAVILENFNTATESDPLGDDFEIFYEYWEKEDPEASQIQYSALSDFADA 1632
Db 1712 LIVNMYIAVILENFNVATESTEPESBDDDFMEYETWEKEDPEATQIFASALSDFADT 1771
Qy 1633 LPEPLRVAKPNKQFLYMDLPMVAGDRLHCDVLFPAFTTRVLGSSGLDTHKTMEEKFM 1692
Db 1772 LSGPLRPKPNQNTLIQMDLPLVPGDKTHCDLILFAFTKNVLGSGGLDLSLKTNNEEKFM 1831
Qy 1693 EANPFKLYEPIVTTTKRKEEOGAAVIQRAYRKHM 1728
Db 1832 ATNLSKASYEPIATLRLKQEDLSATVLOKAYRSYM 1867

RESULT 6

US-08-836-325-7
Sequence 7, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Haleboua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917, 0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-325-7

Query Match 48.8%; Score 4479.5; DB 3; Length 2005;
Best Local Similarity 48.18; Pred. No. 0;
Matches 950; Conservative 276; Mismatches 450; Indels 301; Gaps 38;
Qy 11 PDERNFRPFTSDSLAAIKKRIAOK-----ERKSKDKAAAEQPPRQQLDLKASRKLPK 64
Db 9 PGPDFRFFTRSLAAIEQRIAEKAKRPQERKDEDD-----ENGPKNSDLEAGKSLPF 64
Qy 65 LYGOIPPLVTKPLEDDLPYKDKHTFMVNLKRTIYRFSKAKRALFIIGPNPLSLMIR 124
Db 65 IYGOIPPMVSEPLEDDLPYINKRTIFVLNKGKAIKRSATSALYILTFFNPIKRLAK 124
Qy 125 ISVHSVSMETICTVIIINCMEFMANSMERSFNDIDPEYFVIGIYLEAVIKILARGFVDE 184
Db 125 ILVHSLFNVLIMCTILTNCFVMTSNPPDWTKNV-EYFTGIYTESLIKILARGFCLE 183
Qy 185 FSFLRDPWNWLDIVIGTAIATCFPGSQVNLSALTRFVRFRALKAKAISVISGLKVIVGALL 244
Db 184 FTFLRNPWNWLDFTVITFAYVTEFV- NLGNVSALTRFVRALKTISVIGLKTIVGALI 242
Qy 245 RSVKLVDMVWLTFLCLSFIFALVGOQLFMGILNKKIKHNCNCPASN----- 292
Db 243 QSVKLSVMILTVPCLSVFALIGLQLEFMGNLRNKLQW-----PPDNSTFEINITSPFN 297
Qy 293 -----KDCFEKEKDEDFIMCGTWLGRPCPNMGSTCDKTT 327
Db 298 NSLDWNGTAFNRTVMFMWDEYIEDKSHFYFLEGONDALLCNSSDAGOCPEGYICVRAG 357
Qy 328 LNPNNYTKFNFGMSFLAMFRVMTQDSWERLYRILRTSGTYGIVFFVWIFLGSFYLL 387
Db 358 RPNVGYTSPDTFSWAPLSLFRMLTQDFMENLYQLTLRAAGKTYMIFVVLVFLGSPYLI 417
Qy 388 NLTAVMAYEBOQNVAATEKAKMFQE-AQOLLREKEALVAM----- 433
Db 418 NLILAVAMAYEEQNQATLEAEQKEAFQOMLEOLKQKEAQAAAAAESAESDFSGA 477
Qy 434 -GIDRSSLSLQASSFSFKKFKFGSKTK----- 462
Db 478 GGIGVFSESSVASKLSKSEKELKNRRKKKQKQAGEEKEDAVRKSASEDSIRKKGF 537
Qy 463 SFFMRGSKTAQ-----ASASDEDD- 482
Db 538 QFSLGSLRITYEKRFPSPHQSLLSIRGSLFSPRRNSRASLNFNKGVRKXIDIGSENDFADDE 597
Qy 483 -----ASKNPOLLEOTKRLSONLPV----- 502
Db 598 HSTFEDNDSRDSLFVPHRHGERRPSNVSQASRASRGITPLPMNGKMHSAVDCNGVSLV 657
Qy 503 -----DLFDE-----HV-----DPLHRORALSAVSILTIITQ 529
Db 658 GGPSALTSFVGQLLPETTTETETKRRSSSVHVSMDLLEDP-SQRAMSMASILTNTWE 716
Qy 530 EOEXFQEPFCPCGNLAKSYLVDCSPQWLCKIKVLRITMTDPTTELATITCIINTVFL 589
Db 717 ELESROKQPCPCWKYKFNANCLIMDCCKPWLKVKHVNLVWMDPFDVLAITICIVLNTLFM 776
Qy 590 AVEHHNDDNLKTLIKIGNWVFTGIFIAEMCLKIITALDPYHYFRGNVDFSVALLSLA 649
Db 777 AMEHPMTEQFSSVSLVGNLVFTGIFTAEMFLKIITANDPYTYFQEGMIFDGFIVLSLIM 836
Qy 650 DV-LYNTLSDNNRSFLASRLRVFKAKSWPTLNTLKIIGHSVGALGNLTAVLTIVVF 708
Db 837 ELGLANV---EGLSVLRSFRLRLRVFKLAKSWPTLNLKILIGNSVGLGNLTFLVLAIVF 893
Qy 709 IFSVVGMLRFGTKFNKTAATQ---ERPRRRHMDNFYHSFLVFRILCGEWIENMGCM 765
Db 894 IFAVVGMOLFCKYKCEVCCKISNDCELP-RWHMHFFHSFLIVFRVLCGEIETMDCM 951
Qy 766 QDMGSPLCIIVFLIMVIGKLVNLNLFIALLLNSFSNEEKDGSLEGETRKTQVLAJDR 825
Db 952 -EVAGQTMCLTVFMVMVIGNLVNLNLFALLLSFSSDNL-AATDDDDNNMNLQIAYGR 1009
Qy 826 FRRAFSEFMLHALQSFCCCKKRRKNSP---KPKETTESFAGNKDSILDPARPWKEYDTD 881

Db 1010 MQGIDVKKIRIFQKAFVRKQKALDEIKPLEDLNN-----KDCISN----- 1055
Qy 882 MALYTGQAGAPLAPLAVEDDVEYCGEG---GALPTQSHSAGYQAGD---LPPETKQL 933
Db 1056 -----HTTIEIGKDLNLYKDGNGTTSIGIGSSVEKYVYVDESDFYNNPSLTV 1103
Qy 934 TSP-----DDQGVMEVFSEEDLHLSIQSPRKSDAVSMLSECSITDLNDFRNLOKV 987
Db 1104 TVPIALGESDFENLNTBEFSSS---DMEESKEKLNATSS-SEGSTVDIGAPABGEQPEA 1159
Qy 988 SPKK--OPDRCFKGLSCHLCHTKDRKSPWLVWNIKRTCYQIVKHSFESFIIIFVIL 1045
Db 1160 EPESLEPEACFTEDCVRKPKCCOISIEGKGLWNLKRTCYKIVHNHFEIIVMIL 1219
Qy 1046 LSSGALIFDVNLPSPQVQKELKCTDNITFIPLLEMLKLVAFGRFRYFTSAMWLDLF 1105
Db 1220 LSSGALAFEDIYIBQRTIKTMLEYADKVFTYIFILEMLLKWVAYGQMFETNACWLDLF 1279
Qy 1106 LIVVSVLSL-----MNLPSLKSFRTRLRALRPLRALSQFEGMKVYVYVALISAPAILN 1158
Db 1280 LIVDVSLSVTANALGYSELGAIKSLRTLALRPLRALSREFEGMRVVVNALLGAIPSIMN 1339
Qy 1159 VLVCLIFLWVFCILGNVLSGKRGRCINGTDINNYLDFTEVPRNSOCNI---SNYS--W 1213
Db 1340 VLVCLIFLWVIFISIMGNVLFAGFYHCINYT-IGEMFDVSVVNNYSECQALIESNOTARW 1398
Qy 1214 KVPQVNDVGNVYALLOLVATYKGLWLEINAAVDSREKDEQDPDFEANYLYLVVVFII 1273
Db 1399 KNVKVFNDVGLVLSLLOLVATYKGLWMDIYVAVDSNRVELOPKYEDNLYLVVVFII 1458
Qy 1274 FGSFETLNLFTIGVIIDNFNOQKLGQDIFMTEEQKYYNAMKKGITKPKQKPIRPLN 1333
Db 1459 FGSFETLNLFTIGVIIDNFNOQKKEGGODIFMTEEQKYYNAMKKGITKPKQKPIRPPAN 1518
Qy 1334 KQAFVFDLVTSQVDFVILGLIVNMIIMAESADQPKDKVKTFDILNIAFVIFTEIC 1393
Db 1519 KFGQWVDFVTQKQVDFISIMILICLNMTVMVETDQSQEMTILYINLVVILFTGEC 1578
Qy 1394 LKVFALRQHYFNGMNLFCVNVVLSIISTLVSLR-EDSDISPPPTLFRVVRILARIGRI 1452
Db 1579 VLKLSIRHYFTIGWIFDFVNVVILSVGMFLAELEKTFVS--PLFRVIRILARIGRI 1636
Qy 1453 LRLVRAARGITLFLALMSLPSLNFNIGLLFLVMFYAIFGMSWFSKVKKGSGIDDFIN 1512
Db 1637 LRLIKGAGITLFLALMSLPALEFNIGLLFLVMFYAIFGMSNFAVYKREVIGIDMEN 1696
Qy 1513 FETFTGSMCLCFQITTSAGWDTLLNPMLEA-----KEHCNSSQSDSCQOQIAVYVF 1584
Db 1697 FETFGSMCLCFQITTSAGWDTLLNPMLEA-----KEHCNSSQSDSCQOQIAVYVF 1756
Qy 1565 VSYIIISFLVWNYIAVILENFNTATESEDDPLGEDDFEFIEYVWEKFOPEASQFTOYS 1624
Db 1757 VSYIIISFLVWNYIAVILENFNTATESEDDPLGEDDFEFIEYVWEKFOPEASQFTOYS 1816
Qy 1625 ALSDFADALPEPLRVAKPNKFQFLVMDLPVYMGDRLHCLMDVLFATFTRVLGDSGLDTMK 1684
Db 1817 KLSDFAAALDPLLIARPNKVLQIAMDLPMYSGDRHICLDLILPAFTKRVLGESGEMDALR 1876
Qy 1685 TMEEKFEANPNPKKLYEPIVTTTKRKEEGOGAAVIOQARYKHKHMEKVRLKLDKRS 1741
Db 1877 IOMBERFMASNPKSVEYPIITTLKRKQEEVSAIIVQARYRY---LLQKQKRVSS 1930

RESULT 7

US-09-024-020B-3

; Sequence 3, Application US/09024020B

; Patent No. 6030810

; GENERAL INFORMATION:

; APPLICANT: DELGADO, STEPHEN G.

; APPLICANT: DIETRICH, PAUL S.

; APPLICANT: FISH, LINDA M.

; APPLICANT: HERMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOXIN-SENSITIVE
SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-3

Query Match 47.9%; Score 4394.5; DB 3; Length 1978;
Best Local Similarity 47.2%; Pred. No. 0;
Matches 925; Conservative 294; Mismatches 468; Indels 271; Gaps 37;
Qy 11 PDENRPFPTSDSLAAATKRIATQKERRKSKDKAA-----AEPQPPOLDLKASKRKL 65
Db 9 PGPSFPPTFESLANERRIAESKLLKPPKADGSHREDDSKPKNSDLEAGKSLPFI 68
Qy 66 YGDIPPELVTKPLEDLPYKDKRTFMVNLKRTIYRESAKRALFILGPPNPLSLMIRI 125
Db 69 YGDIPQGLVAVPLEDFDPYILTQKTFVVLNRGKTLFRSATPALYILSPNLRIRIAKI 128
Qy 126 SVHSVSMFTICTVIINCMPMANSWERSFNDIDPEYVIGIYILEAVIKILARGFVDF 185
Db 129 LIHSVFSMIIMCTILTNCFVMTFNSPPWSKNV-EYTFGTIYTFESLKIARGFCIDGF 187
Qy 186 SFLSDPNWMLDFIVGTATATCFPGSQVNLALRTERFVRALKATSVISGLKIVIGALLR 245
Db 188 TFLRDPNWLDFVIMMAYVTEFV-DLGNVSALRTRFRVLRALKTISVPGUKTIVGALIQ 246
Qy 246 SVKLLVDVWVLTLFCLSFALVGQLEFMGILNOKCIKHNCGNPNA----- 290
Db 247 SVKLLSDVMTLVFCLSVFALIGLQFLPMGLNRKNCVWPINFNIESYLENGTRGDFWEYI 306
Qy 291 SNKOCFEKEKSEDFIMCGTWTWLGSRPCPNSTGCTDKTTLNPDNNYTKFDFNGWSFLAMPV 350
Db 307 NNKTFNFMVPGMLPPLLCGNSSDAGCQCEPGCQKAGRNPNYGYTSTFDSWAFALPRL 366
Qy 351 MTQDSWERLYRQILRTSGIYEFVFFVVLFGSSYLLNLTAVVTVMAYEENRNVAETE 410
Db 367 MTQDIWENLYOLTURAAGKTYMFIFFVGSFVLNLLAVAVAMAYEENQATLEBAE 426
Qy 411 AKRMFOE-AQOLLREEKEALVA-----MGIDRSSINSLSQASSF 448

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-0208-4

Query Match 47.9%; Score 4390.5; DB 3; Length 1988;
Best Local Similarity 47.2%; Pred. No. 0;
Matches 928; Conservative 290; Mismatches 469; Indels 281; Gaps 38;

Qy	11	PDERNFRFTSDSLAAIKKRIATIAOKERKSKDKAA-----AEPQRPOLDLAKSKRLPKL	65
Db	9	PGPOSFKFTPELANIERRIAESKLPKADGSHREDDSKPKNSDLEAGKSLPFI	68
Qy	66	YGDIPPELVTRPLEDDPYDHDKTFMVLNKKRTIYRESAKRALFILGPENPLRLSLMRI	125
Db	69	YGDIPQGLVAVPLEDFDYLTQTFVVLNRGKTLRFESATPALYILSPFNLIIRIAKI	128
Qy	126	SVHSVFSMFICTVIINCFMANSWERSFDNDIPEYFVIGIYILEAVIKILARGFVDFE	185
Db	129	LIHSVFSMIIMCTILTNCVFMTSPNPEWKNV-EYTFGTIVTESLVKIIARGFCIDGF	187
Qy	186	SFLRDPWNLDFIVIGTAIATCFPGSQVNLALRTFRFRALKAISVLSGLKIVIGALLR	245
Db	188	TFLRDPWNLDFSIMMAYVTFEV-DLGNVSALRTFRVLRALKTSIVIPGLKTIIVGALIQ	246
Qy	246	SVKLVLDVWMLTFLCLSFALVGQOLFMGLNOKCIKHNCGPNA-----	290
Db	247	SVKLVSDVMLITVCLSVFALIGLQFMGNLRKNCVWPINFNESYLENGTRGFDWEYI	306
Qy	291	SNKQFEKEKSEDFIMCGTWLGRPCPNSTGCDKTTLPNNNTYKDFNCFWSEFLAMPRV	350
Db	307	NNKTFYVPGMLEPLLCNSSDAGCQCEGQCMKAGRNPNVGYTSPDFTSWAFLALFRL	366
Qy	351	MTQDSWERLYRQILRTSGIYFVFVVFVIFLGSFYLLNLTAVTMYAEQNRNVAATE	410
Db	367	MTQDWENLYQLTLRAAGAKTYMIFVLVIFVGSFYLVNLI LAVAMAYEQNQATLEAE	426
Qy	411	AREKHFQE-AQOLREKEALVA-----MGIDRSLSNSLQASFS	448
Db	427	QKEAFFKAMLQKQOEAEQAAMATSACTVSEDAIEEBEGEDGVGSPRSSELSKLSK	486
Qy	449	SPKKR-----KFGSKT-----RKSFPM-----	466
Db	487	SAKERRNRKRKQKQKELSEGEKGDPEKVFKSESDGMGRKRAFRPLPDNRIGRKFSIMNQS	546
Qy	467	-----RGSKTAQASADSE---DDASKN-----	486
Db	547	LLSIPGSPFLSRHNSKSIIFRGPGRFRDPGSENEFADDEHSTVEESEGRDRSLFIPIR	606
Qy	487	-----POLLEQTKR-----LSQNLVLDL	504
Db	607	ARERSSYSGYSGYSCSRSSRIFPSLRSVKRNSTVDCNGVSLIGPGSHIGRLLPVK	666
Qy	505	FDE-----HVDPL-----HRQALSAVSILTTT-IOEQEKFOEP	537
Db	667	IDKAATDSATTEVEIKKKGPSLLVSMQDLASYGKRKDRINSIMSVVNTLVEELEESQRK	726
Qy	538	CFPCGKNLASKYLVWDCSPQWLCIKKVLRTWTDFTELATITICIIINTVFLAVEHHNMD	597
Db	727	CPCCWYKANTFLWECHPYKIKELVINLVMPDFVDLATITICIVLNTLPMAMEHHPT	786
Qy	598	DNLTKILGNWFTGIFIAEMCLKIIALDPVHYFRHGNVNFDSIVALLSLADVLYNTLS	657
Db	787	POFEHVLAVGNLVFTGIFIAEMFLKLIAMDPPYFQEGWNIFDGFIVLSLMEL-----SLA	843
Qy	658	D-NNRSFLASLRVLRFVFLAKSWPTNLTNLIKIHGSVGA LGNLTAVLTVFVIFSVGMGR	716
Db	844	DVEGLSVLRSFRLRVLRFVFLAKSWPTNLTNLIKIHGSVGA LGNLTAVLTVFVIFAVVGMQ	903
Qy	717	LFQTKFNK-TAYATQERPRRHNDNFYHSLVFLVRLICLGEWENNWCCMDMGSPICI	775

9

RESULT

US-08-836-325-11

Qy 1134 RALSOFGMKVVVALISAIPAILNVLVLVLCIFLWLFVLCILGNVLFSGKFGRCINGTIDNM 1193
Db 1299 RALSRFEGMRVVALIGASIMNVLVLVLCIFLWLFVLCILGNVLFSGKFGRCINGTIDGSR 1358
Qy 1194 YLDTVEPNRSOC---NIS-NYSWKYPQVNFNDVGNAYLALLQVATYKGLWLEIMNRAVD 1248
Db 1359 F-PXSQVNRSECFALMNVSXNVRKNNLVNFDNVLGVLVLLQVATYKGLWLEIMNRAVD 1417
Qy 1249 SREDEOPDFEANYLYVYVFFIIFGFFTLNLFVIGVINDFNQOQKKGQDIFMTEE 1308
Db 1418 SVNVXQPKYEYSLYMYFYVXFEIIFGFFTLNLFVIGVINDFNQOQKKGQDIFMTEE 1477
Qy 1309 QKKYNNAMKLGTKKPKQKPIRPNLKNQOAFVDFVLTQSVDFVILGLIVLNMIMMAESA 1368
Db 1478 QKKYNNAMKLGSKPKQKPIRPNLKNQOAFVDFVLTQSVDFVILGLIVLNMIMMAESA 1537
Qy 1369 DQPKDKVKTDFILNIAFVITIECLIKVAFALROHYFTNGWNLFDVGVVLSIIST-LVS 1427
Db 1538 QXXXXXVLXWINKVFIILFTGCVLKLISLRHYFTVGNWIXXFFVVIIXSVIWMFLAX 1597
Qy 1428 RLEDSDISFPPTLFRVRLARIGRILRLVRAARGIRTLILFALMMSLPSLNFILGLLFLVM 1487
Db 1598 XIENYFVS-PTLFRVRLARIGRILRLXKCAKIGRITLLFALMMSLPALENLGLLFLVM 1655
Qy 1488 FIYAIFGNSWFSKYKSGGIDIFNFETFTGSMCLCFQITTSAGWDTLINPMLEA----- 1542
Db 1656 FIYAIFGNSWFSKYKSGGIDIFNFETFTGSMCLCFQITTSAGWDTLINPMLEA----- 1715
Qy 1543 ---KEHCNSSQDSQOQOIAVVFVSVYIIISFLIVNMVYIAVILENFATATESESDPLG 1599
Db 1716 DPKVHGPGSSVGGCGNPSGVIFVSVYIIISFLIVNMVYIAVILENFATATESESDPLG 1775
Qy 1600 EDDFEIFYVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKQFQVMDLPMVMGDR 1659
Db 1776 EDDFEIFYVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKQFQVMDLPMVMGDR 1835
Qy 1660 LHCDVLFAPTRVLGDSGLDTHKTMMEKFMANPKKLYEPIVTTTKRKEEQGAUV 1719
Db 1836 IHCLDILFAFTRVLGDSGLDTHKTMMEKFMANPKKLYEPIVTTTKRKEEQGAUV 1895
Qy 1720 IORAYRHKMKVLRKLDKSSSS 1743
Db 1896 IORAYRRY-----RLRQXVKNISS 1914

RESULT 10
US-09-024-020B-9
; Sequence 9, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024, 020B
; FILING DATE: 16-FEB-1998

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
OS-09-024-020B-9

Query Match 47.1% Score 4316.5; DB 3; Length 1976;
Best Local Similarity 46.8% Pred No. 0;
Matches 915; Conservative 293; Mismatches 478; Indels 269; Gaps 37;

Qy 11 PDERNFRPTSDSLAAIKKRIAIQERKKSKDKAA-----AEPQPRQLDLKASKRLPKL 65
Db 11 PGPSDFKPTPELANIERIAESKLLKPKKADGSHREDDEDSKPKPNSDLKAGKSLPFI 70
Qy 66 YGDIPELVTPLEDDPYKDKHTFVNLKRIYRFSAKRALFILGPNPLSLMRI 125
Db 71 YGDIPELVTPLEDDPYKDKHTFVNLKRIYRFSAKRALFILGPNPLSLMRI 130
Qy 126 SVHSVFSFICTVIINCMENAMNSMERSFNDIDPEYVIGYVILEAVIKILARGFVDF 185
Db 131 LIHSVFSFICTVIINCMENAMNSMERSFNDIDPEYVIGYVILEAVIKILARGFVDF 189
Qy 186 SFLRDPNWLDFIVIGTAIATCFPGSQVNLSALRTRFRVFRALKAISVLSGLKIVIGALLR 245
Db 190 TFLRDPNWLDFIVIGTAIATCFPGSQVNLSALRTRFRVFRALKAISVLSGLKIVIGALLR 248
Qy 246 SVKKLVDMVITLFCISIFALVGQOLFPMGILNKQIKINCGPNPA----- 290
Db 249 SVKKLVDMVITLFCISIFALVGQOLFPMGILNKQIKINCGPNPA----- 308
Qy 291 SNKDFEKEKEDSEDFIMCGTWLGRPCPNGSTCDKTTLPDNNYTKDFNFGKSLAMFRV 350
Db 309 NKNTFYVMPGMLPLICGNSSDAGQC-EGFQCSKAGRNPNYGYTSFDTFSWAFIALPRL 367
Qy 351 MTQDSWERYLQILRTSGIYFVFFVVFVIFLGSFYLLNLTLAVVTMAYEEQNRRNVAATE 410
Db 368 MTQDYWENLYQILRTSGIYFVFFVVFVIFLGSFYLLNLTLAVVTMAYEEQNRRNVAATE 427
Qy 411 AKEMFQF-AOOLREKEALVA-----MGIDRSSUNLSQASSF 448
Db 428 QKEAFKAMLEQLKQOEAEQAAAMATSGATVSEDAIEEGEDGVGSPRSSSELSKLSK 487
Qy 449 SPKKR-----KFFGSKT-----RKSF----- 464
Db 488 SAKERNRKRKRKOKELSEGEKEKDPKVFKESEYGMRRKAFRLPDNRIGRKFSSIMNQS 547
Qy 465 -----FMRGSKTAQASASDSE--DD----- 482
Db 548 LLSIPGSPFLSRHNSKSSIFSGDPSPDRDPCSENEFADEHSTVEESEGRDLSLPIRA 607
Qy 483 -----ASKNPQLLEQTKLSONLPVD-----LFDERHVD 510
Db 608 RERRSSYSGYSGYSCSRSSRISPAQAQREANSTVDCNGVSVSLIGPGSHIGRLLRQLR 667
Qy 511 PLHRQALSAVSILIT-----IQOEKFOEPFCPGKNLASKYL 550
Db 668 WKLRRKALDSFSFGPTLLRTEGONQOHNHGRHGHASEELESORCKPCPCWYKPAFTFL 727

Qy 551 VWDSPQWLCKIKVLRITMDPTFTLAIITCIITVFLAVEHHNDNDLTKILIGNV 610
Db 728 IWECHPYWIKLKEIVNLVMDPFVDLAIICIVLNTLFMAHEHPMTQPEHVLAVGNLV 787
Qy 611 FTGFIAPMCKLIATLDPIYHFRGNWVDSIVALLSLADVLYNTLSD--NNRSLASLURV 669
Db 788 FTGIFTAEMFLKLIAMPYFYFQBGWIFDFGIVSLIMEL---SLADVEGLSLRSPRL 844
Qy 670 LRVEFLAKSWPTLNTLKIIGHSGALGNLTIVLTIVVIFSVVGMRLFCGPKNK--TAYA 728
Db 845 LRVEFLAKSWPTLNTLKIIGHSGALGNLTIVLTIVVIFSVVGMRLFCGPKNK--TAYA 728
Qy 729 TOERPRRWHMDFHFLVFRILCGEWINMMGCMQMDGSLPCIIVFVLMVIGKLV 788
Db 905 NOECKLPRWHMDFHFLVFRILCGEWINMMGCMQMDGSLPCIIVFVLMVIGKLV 788
Qy 789 VLNLFIALLLNSFNE-----EKDGSLEGETRKYVOLALDRFRRAFSEFMLHALQSFCCK 843
Db 964 VLNLFIALLLNSFNE-----EKDGSLEGETRKYVOLALDRFRRAFSEFMLHALQSFCCK 843
Qy 844 KCRKNSPKKETTSEFAGENKOSILP-----DARPKKEYTDMALYTGQAGAPLAPLAE 898
Db 1018 HFKOREADEVPLDEL--Y--EKKANCIANHTGVDIHRNGDFQKNGTTSIGGSVEKYII 1075
Qy 899 VEDDVEYCGEGGALPTSQHSAGVQAGDLPETKOLTSPDQGVEMEVSEEDLHLSIQSP 958
Db 1076 DEHMSFINN---PNTLVTRVPIAVE--SDFENLTED-----VSESSED-----PEGS 1118
Qy 959 RKSDAVSMLESTIDNLNFRNLOKTVSPKO-----PDRCFPKGLSCHFLCHTKDK 1012
Db 1119 KDKLDDTSS--SEGSTIDIKPEVEV---PVEQPEYLDPDACFTGECVORFKCCQVNI 1172
Qy 1013 RKSFWLWNNIRKCYOIVKHSWESFIIIFVILLSSGALFEDVNLPSRQVEKLLRCTD 1072
Db 1173 EEGLGKSWILURKCYOIVKHSWESFIIIFVILLSSGALFEDVNLPSRQVEKLLRCTD 1072
Qy 1073 NIIFTIFELLEMILKWAFFGRYFRTSACWCLDFLIIVVSVLSLM-----NLPSLKSFR 1125
Db 1233 KVFTYIFILEMLLKWTTYGFKVFFTNACWCLDFLIIVVSVLSLM-----NLPSLKSFR 1125
Qy 1126 TLRALRPLRALSQFEGKVVVYALISAIPALLVLLVCLIFLWFCILGNLFSKGFRG 1195
Db 1293 TLRALRPLRALSQFEGKVVVYALISAIPALLVLLVCLIFLWFCILGNLFSKGFRG 1195
Qy 1186 INST--DINMYLDFTEVNRSC-----NLSNYSKVPQVNDVGNAYLALLOVANYKG 1238
Db 1353 FNETSEIRFEDI--VNNKDCXELMEGNSFIRKNNKVNDFNDVGNAYLALLOVANYKG 1410
Qy 1239 WLEINNAVDSREKDEQDFEANYLYFVVFIFIGSFFTLNLFIGVIIDNFNQOQKL 1298
Db 1411 WMDIMYAAVDSRKDEQDFEANYLYFVVFIFIGSFFTLNLFIGVIIDNFNQOQKL 1470
Qy 1299 GGQDIFWTEGOKKYNNAMKLGTKPKQKIPRPLNKCOAFVDFLVTQSVDFVILGLIVL 1358
Db 1471 GGQDIFWTEGOKKYNNAMKLGTKPKQKIPRPLNKCOAFVDFLVTQSVDFVILGLIVL 1358
Qy 1359 NMILMAESADQPKDKVKTFTDILNIAFWIFTIECLIKVVALROHYFTNGWNLFCVVVV 1418
Db 1531 NMVIMVETDQSKOMENILWNLVFIETCECUMKALRHYYFTIGWNIFFVVI 1590
Qy 1419 LSIIST--LVSRLSDSIDSPFTFRVVRVLARIGRILRLVRAARGIRTLFALMMSPLSF 1477
Db 1591 LSIIVMFLADIEKYFVS--PTLFRVIRLARIGRILRLVRAARGIRTLFALMMSPLSF 1648
Qy 1478 NIGLILLVLMFIYAFGMSWFSKVKSGGIDDFENFTFGSMCLCFQITTSAGWDPLN 1537
Db 1649 NIGLILLVLMFIYAFGMSWFSKVKSGGIDDFENFTFGSMCLCFQITTSAGWDPLN 1537
Qy 1538 PMLEA-----KEHCNSSQDSQCOQPIAVVYFVSVYIIISFLVNVNMYAVILENFTA 1590
Db 1709 PILNRPPDCSLDKHPSGSGKDCGNSVGIFVSVYIIISFLVNVNMYAVILENFTA 1768
Qy 1591 TEESDPLGDDDFEIFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKQFLVM 1650

Db 1769 TEESADPLSDEDDFTFEWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKQFLVM 1828
Qy 1651 DLPVMDGRHLCMDVLAFTTRVLGDSGLDTMTMMEKEPMANPFKLYEPIVTTTKR 1710
Db 1829 DLPVMDGRHLCMDVLAFTTRVLGDSGLDTMTMMEKEPMANPFKLYEPIVTTTKR 1888
Qy 1711 KEEBOGAAVIOTARAYKHM-----EKWVKLRKLD 1738
Db 1889 NEEVSAVVUORAIRGLARRGFCIRKMSKNLEN 1923
RESULT 11
US-08-836-325-15
Sequence 15, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Haleboua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Usi
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-15
Query Match 45.68; Score 4185; DB 3; Length 1835;
Best Local Similarity 48.98; Pred. No. 0;
Matches 939; Conservative 266; Mismatches 397; Indels 320; Gaps 64;
Qy 11 PDERNFRPFTSDSLAAIKKRIAIQKRRKSKDKAAAEPPQRPQDLKASRLPKLYGDIP 70

Db 7 PGQSFVFTKQSLALRQ--IEKKEKKD-----DEEPPSSDLEAGKOLPIYGDIP 60
Qy 71 PELVTKPLEDDPYKDKHRTFMVNLKRTIYRFSAKRALFALIGLPENPLRSLMIRISVHSV 130
Db 61 PGWSEPLEDDPYADKKTIVLNKKG-IFRENATPALYMLSPFSLRISIKLVHSL 119
Qy 131 FPMIICITVINCMFMANBERSFNDNPIPEVFIYIIVAVIKILARGFIVDESFURD 190
Db 120 FSLIMCTILNTCFMTPN---PMTKNV--YTFGTIYTFES-LKILARGFCVGBETFLRD 173
Qy 191 PWNMLDFIVCTATATCFPGSOVNLASALRTRFRALKAIISVIGLKVIIVCALLRSVKKL 250
Db 174 PWNMLDFVIVFAYLITEV-NLGNVSALRTRFRVLRALKTIISVPCLKTIVGALIQSVKKL 232
Qy 251 VDMVLTILFCLISIFALYQOQLFMGLNQKCIKHNGCP-----NPAASNKDCFEKEKSDBF 305
Db 233 SDVMILTVECLSVFALIGLQFMGLNKHKCFRLENITLESIMTNESEBEKYFYLEGSKDA 292
Qy 306 IMCGTWLGSRPCNGSTCDKTLTPNDNNYTKFDNFGHSLFAMFRVMTODSWERYLQILR 365
Db 293 LLCGFSTDSGQCPEG-YCVKGR-NPDGYGTSFDTFSWAFALFRMLTQDYWENLYQOFLR 350
Qy 366 TSGIVFVFFVVFVFLGSEFYLLNLTAVVTWAYEEQNRNVAATEAKEMFQEAQOQLR- 424
Db 351 AAGKTYHIFVVFVFLGSEFYLLNLTAVVAMAYEEQNRNVAATEAKEMFQEAQOQLR 410
Qy 425 --EKEALVA-----MGIDRSSLSLQASSPSPKRRKFFGSK----- 459
Db 411 EOEBAEALAAAAETSIRSIRIMGLSESS-SETSLSSKSAKERRNRKQKQSSKEEGKD 469
Qy 460 -----TRKSTFM-----RGSKTA-----Q 473
Db 470 EKLKSSESIRKSPHLGVEGHEKRLSTPNQSPLSIRGSLFSARRSRTSLFSPKGRGD 529
Qy 474 ASASDEDD-----ASKNP----- 487
Db 530 GSETEFADDEHSIFGDNESRRGSLFVPHRPERRSNISOASRSPPLPVNGKMHSAVDCNG 589
Qy 488 -----QLLEQ-----TKRLSONLPVDLDFEHVDPLHRQALSAVSLTITI 528
Db 590 VVSLVDSGSLMLPNCOLLPEGTWQKRSSVYSEDMLN---DPL-RQAMSRASILITWV 645
Qy 529 QEQKFBQPCPCGKNLASKYLWDCSPQWICIKVLRTIMDPTPELAIITICIIINPVF 588
Db 646 BELBESROKCY-----RPAHFLIWNCSPLYWIKFKKIYIVM-DPEVDLAIITICIVLNTLF 699
Qy 589 LAVEHHNMDNLTKILKIGNVFTGIFIAEMCLIIALDPHYHPRHGNVFDSSIVALLS- 647
Db 700 NAMEHHPMTBEEKNVL-AGN-LFTGIFAAEMVLKLIAMDPEYFQVGNIFDSLIVTSL 757
Qy 648 ---LADVLYNTLSDNNRSFLASRLVRLVKLAKSWPTLNTLKIIGHSVGALGNLTVVLT 704
Db 758 ELFLADV-----EGLSVLSRFLRLRVFKLAKSWPTLNLMLIKIIGNSVGALGNLTIVLA 810
Qy 705 IWVTFISVGMRLFGTKFNKATAYAQE-RPRRRHMDNFYHSLVFRILCGEWIENMWG 763
Db 811 IIVFIFAVVGMOLFCKSKYKCVCKINDCLP--RWHMNDFFHSLFVFRVLCGEWLETWMD 868
Qy 764 CMQMDGSPCLIIIVFLIWLIVGLVNLNLFALLNLSFNEEKDGLSLEGERTKTKVQVAL 823
Db 869 CME--VAQOMCLIVVMYVWVGNLVLNLFALLLSFSSDNLTAAIEDDANNLQIAVRI 926
Qy 824 DRFRRAFSLMLHALQSFCKCKRKNSPKKET--TESFAGENKDSILDPARPWKYD-- 879
Db 927 ----KGINYQVTLREFILFESKPKPSDNKKENYISNTLAKMSKHNF-----KERDIS 976
Qy 880 -----TDMALYTGQAGAPLAPLAEVEDDVEYCGEGGALPTSQHSAGVQAGDLPPEPKOL 933
Db 977 GGSSDKMDOSFIHNPSTLVTVPIAPGESDLEM-----NEEL 1012
Qy 934 TSPDDQGVEMEVFSEEDLHLSIQSPRKSDAVSMLSEGSTIDLNDIFRNLOKTVSPKQP 993

Db 1013 SSDSD-----SYSKNRSS-----SEGSTVDNPLPGEGEBAEAPNDP 1051
Qy 994 DRCPKGLSCHFLCH-KTDRKSPWLVWNNIRKTCYQIVKHWSFESFIIFVILLSSGALI 1052
Db 1052 EACFTDGCVRRCOVNSGCKG-----WW-IRKTCY-IVHWSFESFIVLWILLSSGALA 1104
Qy 1053 FEDVNLRSRPOVEKLLRCTDNIFTIFILLEMILKWAFFGRFRYFTSANCWLDLFLVVSV 1112
Db 1105 FEDIYI-EKRTIKIILEYADKIYFIIFILEMLLKW-AYGYKTYETNAMCWLDLFLVDVSL 1162
Qy 1113 LSLM-----NLPLSKSFRTLRLALRPLRALRALSOFEGKMKVYVALISATIPALNLLVCLL 1165
Db 1163 VTLVANLTGYSDLGPIKSLRTLRLALRPLRALRALSOFEGKMKVYVALISATIPALNLLVCLL 1222
Qy 1166 FWLVFCILGVNLFSGKFGRCINGTDINNMYLDFTEVPNRSQC-----NITSNYSWKVPQVNF 1221
Db 1223 FWLIFSIMGVNLFAKGYEC-NTTDGSR---FPQVNRSECFALMNVSNVRWKNLKVNF 1278
Qy 1222 NVGNAYLALLOVATYKGLHETMNAAYDSREKDEQDPEANLYAYLYFVVFIFIGSFFTLN 1281
Db 1279 NVGLGYLSLLQVATFGW--IMYAAVDS--VNVQPKYEYSLYMYIYF-VFTIGSFFTLN 1333
Qy 1282 LFIVGIIDFNQOQKLLGGQDIEMTEOKKYNAWKKLTGKPKPIPRPLNKQOAFYD 1341
Db 1334 LFIVGIIDFNQOQKLLGGQDIEMTEOKKYNAWKKLTGKPKPIPRPLNKQOAFYD 1392
Qy 1342 LVTQVEDVITLGLIVLNMIMMAESADQPKDKVKTEDILNI-APVVIETIECLIKVPAL 1400
Db 1393 L-TNOAFDIIV-LICLNMVTMMVEKEGQ-----VLWINVFIILFTGECVLKLISL 1442
Qy 1401 RQHFETNGWNLFDVWVVLSTLVSRLSDSDISFPPTLFRVVRVLARIGRILRLVRAAR 1460
Db 1443 RHYFTVGNWTF--VVVISIVGMFLA----IEYFVSPTLFRVIRLARIGRILRL-KGAK 1494
Qy 1461 GIRTLLPALMSLPSLNFILGLLFLVMEFIYALFGMSWFSKVKKSGIDDIENFETGSM 1520
Db 1495 GIRTLLPALMSLPSLNFILGLLFLVMEFIYALFGMSWFSKVKKSGIDDIENFETGSM 1553
Qy 1521 LCLFQITTSAGMDTLLNPMLEA-----KEHCNSSSDSCQOQPIAVVYFVYIIISFL 1573
Db 1554 ICLFQITTSAGMDGLLAPILNPPDCPKVHPGSGVEGDCGNPSVGIFYFVYIIISFL 1613
Qy 1574 IVWNYTAVILENNTATESEDEPLGEDDFEIFYEVWEKFPDEASQFTQYSAISDFADAL 1633
Db 1614 VVWNYTAVILENNTATESEDEPLGEDDFEIFYEVWEKFPDEASQFTQYSAISDFADAL 1672
Qy 1634 PEPLVAKPNKFOFLVMDLPMVMDRLHCDVLFATFTRVLGDSGLDTMTMEEKPME 1693
Db 1673 DPPLLIAKPNKVQLIAMDPLPMVSGDRIHCLDILFAFTKRVLGEGE-MDSLSRQMEERPMS 1731
Qy 1694 ANPEKKLYEPIVTTTKRKEEBOGAIVQIARVKKHMEKVK-----LRLKDRSSSSHOVF 1747
Db 1732 ANPSKVSVEPIVTTTLKRAQEV--SATIQARVRLRQVKNLISSIIYIKGDRDDDLNKNDF 1789
Qy 1748 CN 1749
Db 1790 DN 1791

RESULT 12

us-08-793-3

Sequence 3, Application US/08808793

Patent No. 5858713

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Ingles, Patricia J.

TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

Db 1524 MYLVFFVFIIGSFTLNLFVGIIDNPNQKKAGGSLEMFMTEDQKYYNAMKMGSK 1583
Qy 1323 KQKPIRPLNKKCAFVDFLVTQVDFVILGLVLNMIIMAAESADQPKDVKKTFDILN 1382
Db 1584 KPLKAIPRWRPQAIIVEIVTDKKFDIIMLFGLNKNFTWLDYDASEAYNNVLDKLN 1643
Qy 1383 IAFVVIETIECLIKVAFALROHYFTNGWNLNDCVWVVIISITLVSRL-LESDISFPPTLF 1441
Db 1644 GIFVIFSGECLLIKAFALRVHYHFKPWNLFVWVILSLGLVLSDIIEKYFVS--PTLL 1701
Qy 1442 RVVRLARIGRLRLVRAARGTIRTLIFALMMSLPSLFNIGLILFLVMEIYAFHGSWFSKV 1501
Db 1702 RVWRAVGRVRLVUGAKGIRTLIFALMSLPALFNICLLFLVMEIFAIFGNSFMHV 1761
Qy 1502 KKGSGIDDFNFETFTGSMCLFOITTSAGWDTLLNPMLEAKHCNSSOD-----SQOQ 1556
Db 1762 KEGSGINAVNFKTFGOSMILLFOMSTAGWDGVLDAIIN-EEDCDPPDNCKGYPGNGS 1820
Qy 1557 PQIAVTVFVYIIISFLIVNMVYIAVILENFTATESEDPLEDDFEIFVYVWEKFDPE 1616
Db 1821 ATVGITELLSVLISFLIVNMVYIAVILENYSQATEDVQEGLTDDYDMYIEIWQFDPE 1880
Qy 1617 ASQFIQYALSDFADALPEPLRAVAKPNKFQFLVMDLPMVWCDRLHCHMDVLFATFTRVLGD 1676
Db 1881 GTQVIRYDQSEFLDVLEPPLOIHKPNKYIISDMNPICRGDMYICVDILDALTKDFFAR 1940
Qy 1677 SSGLDTKMMEEFMEANPEKPIEPIVTTTKRKEEEOGAAVTORAYRKH 1727
Db 1941 KG--NPITEGEIGEIAARPDTEGDPVSSTLWRQREYCAKLIONAWRRY 1989

RESULT 13
US-08-772-512A-3
; Sequence 3, Application US/08772512A
; Patent No. 6022705
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Knipple, Douglas C.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
; TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
; TITLE OF INVENTION: FLIES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,512A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,618
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Branman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/601(CRFD-1657)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2105 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-772-512A-3
Query Match 38.7%; Score 3554.5; DB 3; Length 2105;
Best Local Similarity 38.4%; Pred. No. 0;
Matches 780; Conservative 357; Mismatches 533; Indels 361; Gaps 39;
Qy 9 IFPPERN-FRPFTSDSLAAKKRIATIAOKERKKSKDKAAAE-----PQRPQ 53
Db 8 ISEERSLFPTRESLQTEQRIAEHEKQERKRAAGEQIRYDEDEDEQPDPT 67
Qy 54 LDKASKKLPP---KLYGDIPPELVTKPLELDLPYVKDQKTFMVLNKKRTIYRFSAKRALF 110
Db 68 LE-----OGVPVPMQSGFPPELASTPLEDIDPFYSNVLFVVISKGDIFRFSKAMW 123
Qy 111 ILGPNFLRLSIRISVHVSFMFICTVIINCMMFMSMERSFDNDPIEYVFIGIYLE 170
Db 124 LLDPENPTRRVAIVLVHPLFSLFIITLTNCLIMI--MPTTPTVESTVEITGIVTFE 181
Qy 171 AVIKILARGFIVDFSEFLRDPWNWLDIVIGTATATCFPGSQV--NLSALRTFRVFRALKA 229
Db 182 SAVKVMARGFTLCPFTYLRDAWNWLDVFVIALAYVTM--GIDGLNLAALRTFRVLRALK 239
Qy 230 ISVTSGLKIVGALLRSVKLVDMVWLTFLCLSFALVGQOLFNGILNOKCIK----- 282
Db 240 VAVPGLKTVGAVIESVKNLRVIIITMPSLVSFALMGLOIYMGVLTKCKIKRFPDGS 299
Qy 283 -----HNGCPNPASNKDCFEKEKDEDFIMCGTWLGSRPCNGSTC-DKTTINP 330
Db 300 WGNLTDENWFLHN-----SNSSNWFTENDGESYPCVGNVSGAGCGEDYVLOGFGPNP 353
Qy 331 DNNYTKEDNFGWSFLAMPRVMTQDSWERLYRQILRTSGIYVFFVVFVIFLGSYLLNLT 390
Db 354 NYDYTSDFSFGWAFLSAFLMTQDEWEDLYQHVLQAAGPHMLFFIIFLGSYLVNLI 413
Qy 391 LAVVTMAVEQNRVNAATEAKKMFQEAQOLL----- 423
Db 414 LAIVMSYDELOKKAEEEAEEBAIREAEEAAKAAKLEERANVAQAQAADAAAA 473
Qy 424 -----REKEALVAMGIDRSSLN----- 441
Db 474 ALHPMAKSPYISYELFVGEGKNDNKNKMSIRSVESVESVIOQPAPTAP 533
Qy 442 -----SLQASSFPKK-----RKFFG--SKTKRSPFMRGSKTAQA 474
Db 534 ATKVRKVSTTSLSLPGSPFNLRGSRSSHKYTIIRNGRGRFGIPGSDRKLVLQTYQDAQ 593
Qy 475 SASDSEDDASKNPQ----- 488
Db 594 HLPYADDSNAVTPMSEENGAIIVPAYCNLGRSHSSVTSYSHOSRISYTSHGDLGMAAMG 653
Qy 489 ---LLEQTKRLSON-----IQEQKFQEPFCPCGKNLASKYL 550
Db 654 ASTWKESKLSRNRTRNQSICGAATNGSSSTAGGYPDANHKQORYEMGQDYTDGAKIK 713
Qy 508 -----HVDPLHRQALSVAISLTIT-----IQEQKFQEPFCPCGKNLASKYL 550
Db 714 HHDNPFIEPVQTVQVDMKDVMLNDIIEQAAGRHSRASERGEDDEGPTFKDIALEYI 773
Qy 551 -----VWDCSPWLICIKKVLRTIMTDPTELATITCIILINTVFLAVEHHNDDNLT 602
Db 774 LKGEIFCWDCCWVWLKFQEWVSFIVDPPELVFELTICIVNTMFMAMDHMDNPELEK 833
Qy 603 ILKIGNVFTGIFTAEMCLKIIALDPVYFRHGNWVDSIVALLSLADLVNTLSNNRS 662
Db 834 VLKSGNYFTATFAIEASMKLMSPKYYFQEGNIFEDFIIVALSLELGEV--QGLSJ 891
Qy 663 FLASLRVLRVFKLAKSWPTLNTLTKIIGHSVGLNLTIVVTFISVGMRLFGTKF 722
Db 722 ----- 722

APPLICATION NUMBER: US/08/772.512A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/608,618
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/601 (CRFD-1657)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-772-512A-4

Query Match 38.7%; Score 3550.5; DB 3; Length 2104;
Best Local Similarity 38.4%; Pred. No. 0;
Matches 779; Conservative 357; Mismatches 534; Indels 361; Gaps 39;

QY	9	IFPDERN--FRPSTSLAAIKKRTAIOKERRKSKDKAAAE-----POPRQ 53
DB	8	ISEERLFRPFTRESLQIQRIAEHEKLEKRAAGEQIRYDDEDEDEGPQDPPT 67
QY	54	LDLAKSRKLP---KLYGDPPELVTKPLEDDPYKHDKTFWLNKRTIYFSAKRALF 110
DB	68	LE---QGVPIPVRMQGFPELSTPLEDIDPYVNLTFVVISKDKIDFRFSKAMW 123
QY	111	ILGPNPULRSIMRISVHSMFICTVIINCMPMANSBERSFNDIPEYVFTGIYLE 170
DB	124	LLDPFNPIRVAIYLVHPLFSLFTIITLNCILMI--MPTTPTVESTVFTGIYTF 181
QY	171	AVIKILARGFIVDEFSLRDPNWLDFIVIGTATATCFPGSQV--NLSALRFRFRALKA 229
DB	182	SAVKMARGFILCPFTYLDANWLDFVIALAYTM--GIDGLNLALRFRVRLAKT 239
QY	230	ISVIGLKIVGALLRSVKLVDMVLTFLCLSFALVGQOLFGLNOKIK-----282
DB	240	VAIYPLKTIIVGAVIESVKNLRDVLITMFLSVFALMGLIYMGVLTKQKIKRPLDGS 299
QY	283	-----HNCGNPNANKDCEKEKDESEDFIMCGTWLGRPCPNGSTC--DKTTLNP 330
DB	300	WGNLTDENWFLHN-----SNSSNWFTENDGESYPVCNVSGAGCGEDYVCLQGFNP 353
QY	331	DNNTKEDNFGWSFLAMFRVMTQDSWERYLQILRTSGIYFVFFVVFVFLGSEYLLNLT 390
DB	354	NYDTSEDSFGWAFSLFRMTQDFWEDLYQHVLOAAGPWHMLFVIIFLGSFYLVNLI 413
QY	391	LAVTMYAEQNRNVAAETAKEMFOAQOLL-----423
DB	414	LAIIVMSYDELQKAEBAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 473
QY	424	-----REEKEALVAMGIDRSSN-----441
DB	474	ALHPMAKSPYSCISYELFVYGEKGDNDNNKKNRSRSEVESVSIQRPAPTAP 533
QY	442	-----SLQASSFSPKK-----RKFFG--SKTRKSPFRMRSKTAQA 474
DB	534	ATKVKYVSTLSLPGSPFNLRGRSRSHKTYTIRNGRGRFGIPGSDRKLPLVLYQDAQ 593
QY	475	SASDESDASKNPQ-----488
DB	594	HLPYADDSNAVTPMSEENGAIIVPAYCNLGRSHSYTSHQSRISYTSHGDLLOGMAWG 653
QY	489	---LLEQTKRULQN-----LPVDFDE-----507

DB	654	ASTMTKESKLSRNRTRNQSIGAATNGSGSTAGGYPDANHKEQRDYEMGQDYTDAGKIK 713
QY	508	-----HVDPLHRORALSAVSILTT-----IQOEKKEPCEPCGKKNLASKYL 550
DB	714	HHDPFIEPVQTVVDMKQVWLNDIEQAAGRHSRASEGEDDEDEGPTFKDIALEYI 773
QY	551	-----VMDSPQWLCIKKVLRTITDPTTELATITCIINTVFLAVEHNNDDNLT 602
DB	774	LKGTEIFCVWCCWVWLKQFQWVSFIVDFVELFITLCIVVNTMFMAMDHDMPELEK 833
QY	603	ILKIGNVFTGIFTAEMCKLIIDLPYHFRHGNVFDISVALLSLADLVNLTSDNRS 662
DB	834	VLKSGNFFATFAIEASMKLMAMSPKYFQEGWNIFDIIIVALSLELGEV--QGLS 891
QY	663	FLASLRVLFKLAWSPTLNTLKIIGHSVGALGNLTVLTIVFISVVGMRFGTKF 722
DB	892	VLSRFLLRVFKLAKSWPTLNLISIMGRTMGALGNLTFVLCIIFIFAVGMOLFGRNY 951
QY	723	--NKTAVATQERPRRRHMDNFYHSFLVVRILCGEWENMGCMQDMGDSPLCIIIVFL 780
DB	952	IDHKDFKDHLP--RWNFTDFMHSFIVFRVLCGEWLESWDMCMYGVDSV--CIPFLA 1007
QY	781	IMVIGKLVVNLFIALLNLSFNEEKSGLEGETRKTQVLAALDRFRRAFSMLHALQSF 840
DB	1008	TWVIGNFVVLNLFALLLSNFGS-----SSLSAPTADNDNTKIAEAFNRIARFNKVRNI 1063
QY	841	--CCKKCRK---NSPKPKETTESFAGENKDSILPDAPWK-----EYDTMALYTGQAG 890
DB	1064	ADCFKLIRNLTNISDQPSHGDNELGHDEIMGDLIKKGMKGETQLEVAIDGMEF 1123
QY	891	APLAPL-----AEVEDD-----VEYCGGG 910
DB	1124	TIHGMKNKPKSKFINNTTMTIGNSINHQNRLHELNHRLGLSIQDDDTASINSYSGHK 1183
QY	911	ALPTSQHSAGVOAGDLPPEPKOLTSPDQGVEMEVSEEDLHLSISQSPRKSDAVMSLE 970
DB	1184	NRPFDESHKSAETIEGEEKRDSKEDLGE-----DEEDEAEGDEGLDGDIIHA 1237
QY	971	CSTIDLNDIFRNLOKTVSPKQPCPKGLSCHFLCHKTDRKSPVWLNWIRKTCYQI 1030
DB	1238	QNDDEIIDDY-----PADCFPSYKKFPILAGDEDSFPWCGWGNLRLKTQL 1285
QY	1031	VKHSWFSFIIIFVILLSSGALFEDVNLSPRQVEKLLRCDNTIFTTFLEMLKWWAF 1090
DB	1286	IENKYETAVITMILMSSLALAEVDHLPDRPVMDILYMDRIFTVTFLEMLKWWAL 1345
QY	1091	GFRYFTSAWCWDLFIVVSVLSLM-----NLPSLKSFTLRALRPLRALSQFEGMK 1143
DB	1346	GKVFYFTNMCWDLFIVVLSLNLVAVWSGLNDIAVFRSMRTLRALRPLRAVSRWEGMK 1405
QY	1144	VVYVALISAIPAILNVLVCLIFWLVFCILGVNLPFGKFGRCINGTIDNMVLDTEVNR 1203
DB	1406	VVVALQVAIPSIENVLVCLIFWLVFAIMGVQLFAGYFKCKDGN--TVLSHEIIPNR 1463
QY	1204	SQCINISYSWKVPVNDVNGVNALLOVATYKGLWLEIMNAADVDSREKDEQPOFEANLY 1263
DB	1464	NACKSENVTWNSAMNEDHGVNAYLCFQVATFKGQIIMDAIDSDREVDQPIRETIY 1523
QY	1264	AYLVFVFIIFGSPFTLNLFIIVIDNPNQOKKLGG--DIFMTEQKKYNNAMKLGTK 1322
DB	1524	MYLVFVFIIFGSPFTLNLFIIVIDNPNQOKKLGG--DIFMTEQKKYNNAMKMGSK 1583
QY	1323	KPQPIRPLNKKCAFVDFVTSQVDFVILGLVILNMIIMMASADQPKVKKTFTDLN 1382
DB	1584	KPLKAIPRRWRPQAIIVEIVTDKFDIIMLFIGLNFTMTLDRYDASEAYNVLDKLN 1643
QY	1383	IAFVVIETECILKIVFALRQHYFTNGWNLFCVWVVSIIISTLYSR--LEDSIDISFPPTLF 1441
DB	1644	GIFVVFSGECLLKIIFALRYHYFKPEPNLFDVVVVISLGLVLSIDIEKTFVS--PTLL 1701
QY	1442	RVVRLARTGLRLVRAARGIRTLALLLMMSLPFLNIGLLFLVMFIYAFGMSWFSKY 1501
DB	1702	RVVRVAKVGRVLRVKAGKIRTLALLLMMSLPFLNIGLLFLVMFIYAFGMSWFSKY 1761

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 26, 2002, 22:49:55 ; Search time 72.7 Seconds
(without alignments)
1849.355 Million cell updates/sec

Title: US-09-646-224A-2
Perfect score: 9173
Sequence: 1 MEERYYPVIFPDNERFRPFT.....VFCNGDLSLDVAKVKVHND 1765
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9157	99.8	1765	2 T42388	sodium channel alp
2	4724	51.5	2019	2 A33996	sodium channel pro
3	4711	51.4	2016	2 A38195	sodium channel pro
4	4553	49.6	1977	2 S4771	sodium channel alp
5	4545	49.6	1957	2 S68453	sodium channel pro
6	4501	49.1	2005	2 A46269	sodium channel alp
7	4496	49.0	1951	2 S00320	sodium channel pro
8	4489	48.9	1983	2 A60054	sodium channel pro
9	4484	48.9	2005	2 B25019	sodium channel pro
10	4476	48.8	2009	2 A25019	sodium channel pro
11	4363	47.6	1840	1 CHRTM1	sodium channel pro
12	4355	47.5	1836	2 I64893	sodium channel alp
13	4347	47.4	1836	2 I51964	sodium channel alp
14	4342	47.3	1836	2 J50648	sodium channel alp
15	4331	47.2	1835	2 I54323	sodium channel alp
16	4316	47.1	1976	2 I36555	sodium channel pro
17	3983	43.4	1820	1 CHEE	sodium channel pro
18	3518	42.7	2049	2 T43161	sodium channel pro
19	3554	38.7	2108	2 S72458	sodium channel pro
20	3512	38.3	1784	2 T43167	sodium channel pro
21	3479	37.9	1993	2 T30902	sodium channel SCA
22	3242	35.3	1820	2 A33299	sodium channel pro
23	3184	34.7	1682	2 A45380	sodium channel pro
24	3032	33.1	1689	2 S72467	sodium channel pro
25	3021	32.9	1681	2 A55138	sodium channel mRNA
26	3016	32.9	1699	2 T31340	voltage-gated sodi
27	2959	32.3	1810	2 T31092	probable voltage-g
28	2945	32.1	1522	2 JC1101	sodium channel pro
29	2732	29.8	1321	2 A60165	sodium channel pro

ALIGNMENTS

RESULT 1

T42388

sodium channel alpha chain - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T42388

R:Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.

Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998

A:Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in perip

A:Reference number: 222149; MUID:98338024

A:Accession: T42388

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1765 <DIR>

A:Cross-references: EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC40199.1

A:Experimental source: strain Sprague-Dawley; dorsal root ganglia

A>Note: preferentially expressed in sensory neurons within dorsal root ganglia and t

C:Superfamily: sodium channel protein

Query Match 99.8%; Score 9157; DB 2; Length 1765;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1761; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEERYYPVIFPDNERFRPFTSDSLAAIKKRIAIQKERRKSKDKAAAEOPRQOLDLKASR 60

DB 1 MEERYYPVIFPDNERFRPFTSDSLAAIEKRIAIQKERRKSKDKAAAEOPRQOLDLKASR 60

QY 61 KLPLKLYGDIIPPELVTKPLEDLDPYKDKHKTVMVLRKRTIYRFSAKRALFILGPNPLRS 120

DB 61 KLPLKLYGDIIPPELVAKPLEDLDPFYKDKHKTVMVLRKRTIYRFSAKRALFILGPNPLRS 120

QY 121 LMRISVHSVSMFICTVIINCMPMANSERSFONDPIEYVFIGIYILEAVIKILARGF 180

DB 121 LMRISVHSVSMFICTVIINCMPMANSERSFONDPIEYVFIGIYILEAVIKILARGF 180

QY 181 IVDESFRLDPNNWLDIVIGTAIATCPGSOVNLISALRTFVRFRALKAISVISGLKIV 240

DB 181 IVDESFRLDPNNWLDIVIGTAIATCPGSOVNLISALRTFVRFRALKAISVISGLKIV 240

QY 241 GALLRSVKLVDMVMTLFLCSIFALVGQQLFMGLINQKCIKHNGCPNPASKNDCFEK 300

DB 241 GALLRSVKLVDMVMTLFLCSIFALVGQQLFMGLINQKCIKHNGCPNPASKNDCFEK 300

QY 301 DSEDFIMCGTWTGSRPCPNSTCDKTTLMNDNNYTKFDNFGWSFLAMFRVMTQDSWERY 360

DB 301 DSEDFIMCGTWTGSRPCPNSTCDKTTLMNDNNYTKFDNFGWSFLAMFRVMTQDSWERY 360

QY 361 RQILRTSGIYFVFFVWVIFLGSFYLLNLTAVVTMAYEQNRNVAATEAKEMFQEAQ 420

DB 361 RQILRTSGIYFVFFVWVIFLGSFYLLNLTAVVTMAYEQNRNVAATEAKEMFQEAQ 420

Dd	1360	GKFGRCINQTEGDLPLNYTIVNKKSECSFNWYTGELVTKVKVFNDNVNGAGYLALLOVAT	1419
Qy	1236	YKGWLEITMAAAYDSREKDEQPQFEANLAYLYFVVFIIFEGSFFTLNLFIGVIIDNFNQOQ	1295
Dd	1420	EKGMDIMYAANDSRGYEQPQEWEDNLYMYIFYVVFIIFEGSFFTLNLFIGVIIDNFNQOQ	1479
Qy	1296	KLGGGDIFMTBQBKKYYNAMKLGKTGPQKPIRPLPNKCQAQVFDLVTSOVDFVILGL	1355
Dd	1480	KLGGGDIFMTBQBKKYYNAMKLGSKKPQKPIRPLPNKYQGIFDIVTKOAFDVTJMLF	1539
Qy	1356	IVLNMIIAMAESADQPKDYKKTFTDILNTAFVVIPTIECLIKVFALRQHYPFNGHNLFCV	1415
Dd	1540	ICUNMVMVETDDQSPEKVNTAKINLLVAIFTGECIVKMAARHYEFTNSWNIEDFV	1599
Qy	1416	VWLSIISTLVSRLEDSDISFPPTLFVRVRLARIGRILURLVRAARGRTTLLFALUMSLPS	1475
Dd	1600	WVLSIGTVLSLDIOK-YFFSPTLFVRVRLARIGRILURLIRGAKGIETLLFALUMSLPA	1658
Qy	1476	LFNIGLLLFLVMFYIAIFGMSWFSGKVGSGIDDIFNETFTGSMCLCFAQITTSAGWDTL	1535
Dd	1659	LFNIGLLLFLVMFYISIFGMANFAVYKWEAGIDDMENFOTFANSMLCFAQITTSAGWDGL	1718
Qy	1536	LNPMLE-AKEHC-----NSSQSDSCQQQPIAVYVFSYIIISPLVVNMVYIAVILENPN	1588
Dd	1719	LSPILANTPPCYCDNPINPSNGRGNCSPAGVILFETTYIISELVVNMVYIAILENFS	1778
Qy	1589	TATEESDPDGDDFEIFYEVMEKEDPEASQFIQYSALSDFADALPEPLRVAKENPKQEL	1648
Dd	1779	VATEESTEPUSEDFOFMFEIMEKEDPEAQFIETLUSDFADALSEPLRIAKENQISLI	1838
Qy	1649	VMIDLPMVWGDRLHCMVDLFAFTTRVLGDSGDLDTMKTMAMEEKMEANPFKKLYEPIVTTT	1708
Dd	1839	NMDLPWVSGDRIHCMIDLFAFTKRVLGESGENDALKIQMEESKEAANPSKSYEPIITTL	1898
Qy	1709	KRKEEEOGAATVIOARYKH-MEKWKV 1733	
Dd	1899	RRHEEVSATVIOARFRHLLORSRK 1924	

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RESULT      3
A38195
N:sodium channel protein hHI, cardiac - human
C:Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
K:Accession: A38195
R:Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barch,
proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A>Title: Primary structure and functional expression of the human cardiac t
riggered by angiotensin II receptor stimulation.
P:Reference number: A38195; MUID:92115699
A;Accession: A38195
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A;Residues: 1-2016 <GEL>
A;Cross-references: GB:M77235; NID:g184038; PIDN:AAA58644.1; PID:g184039
A;Experimental source: heart
A;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport
Query Match          51.4%; Score 4711.5; DB 2; Length 2016;
Best Local Similarity 50.2%; Pred. No. 0;
Matches 970; Conservative 281; Mismatches 435; Indels 247; Gaps
Qy 15 NFRRPTSDSLAAIKRIATOKER-----KKSKDKAAAEQPQRQLDLKASRKLPKLVGYDI 69
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Zb 12 SFRRFTRESLAATEKRMAEKQARGSTTLQESREGLPPEEPAPRPQLIDLQAASKLPDLYGNP 71
    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 70 PPELVTPKLEDDPPYVKDHKTFWNLKNKRTIVRFSAKALFLILGFNPRLSRIMIRISVHS 129
    |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 72 PQEIGEGLDEDDPFYSTQTKTIFVLNNKGITIFRESALTNALYGSFPHPVRRAAVKLIVHS 131
    :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Qy 130 VFSWFICTVIINCMPMANSMSERSFNNDIP-----EVVFIGIYLEAVIKLAGFIIVD 183

```


QY	11	PDERNRPPTSDSLAAIKRRIAIQKBERK-KSKDKAAAEPQPRPQLDUKASRKLPKLKYVDI	69
Db	7	PGQSFVHFTKQSALIEQRIARSKSEKPEEKEDDDDEAPKPSDSLEAGKQLPFYIGDI	66
QY	70	PPELVTKPLEDLDPYYVKOHKTWFLWNKKRTIYFESAKALFTILGPNPLRLSMLIRISVHS	129
Db	67	PPGWSEPLEDLDPYTADKKTIYLINKGTFIFRENATPALYMLSPFPRLRISIKILVHS	126
QY	130	VFSHFICTIVINCMPMANSERSFDNDPIEYVFYIGIYLEAVIKILARGDIVDFSEFLR	189
Db	127	LFSMLIMCTILTNCIPMTNNPDMTKNV-EYTFGTIVTESLSVKILARGCVCEFTFLR	185
QY	190	DPNNWLDFIVIGTAIATCFPGSQVNLSALTRFRVRPAKKAISVSGLKVIYGALLRSVKK	249
Db	186	DPNNWLDFVVIYFAYITEFV-NLGNVSALTRFRVLRAUKTISVIPGLKTIYVALIOQVKK	244
QY	250	LVDVWLTLFCLSIPALVGQOLFPMGLNCKCIKHNGCNPNA-SNKDCFEKEKD-	301
Db	245	LSDVMILTVCFLSVFALIGLOLFPMGNLHKHCERNLENNETLESIMNTLESEEDFRKYFY	304
QY	302	-----SEDFTMGCTWLGSRPCPGNSTCDKTTLNPDNNYTKFDNFWSFLAMFRVMTQDSWE	357
Db	305	YLEGSXDALLCGFSTDSGOCPGYTCVIGRPNPDYGYTSFDTESWAPLALPRLMTQDYWE	364
QY	358	RLYROILRTSGIYVEFFVVVIFLGSFYLLNLTLAVTWIYBEEQNRVVAATEAKEMFO	417
Db	365	NLYOOTLRAGAKTYMTIFFVVVIFLGSFYLLINILAVAMAYEQNANIEEAKOKELEFO	424
QY	418	EAOOLLR---EKEELAVA-----WGIDRSSLSIOASSFSFKPKRKFEGSK--	459
Db	425	QMLDRLLKKQEBAEAIAAAAAEYTSIRRSRINGLSESSETSKLSSSAKERRRNRKKKN	484
QY	460	-----TRKSFFM-----	466
Db	485	QKKLSGEEKGDAEKLKSESDSIIRKSFHLGVGBGHRAHEKRLSTPNQSPLSIRGSLF	544
QY	467	----RGSKT-----AQASASDSE-----DDASKNPOL-----LEQ	492
Db	545	SARRSRTSLFSFGKRGRDIGSETEFADDEHSIFGDNESRGSLFPHRPOERRSSNIQ	604
QY	493	TKRLSONLPVD-----	505
Db	605	ASRSPMLPVNGKMHSAVDCNGVSVLDGRSALMLPNQQLPEGTTNQIHKKRCSSYLL	664
QY	506	DEHV-DPLHRQRALSAYSILITITOBEKQFOEPCPGCNLAISKYLVWDGCSQMWLCIKK	563
Db	665	SEDMLNDPNLRQAMSRA SILNTVEELESROKCPPWWYFAUHKFWLWCNSPYWIKFKK	724
QY	564	VLRTIMTDPELATAICIIINTVFLAVEHHNMDDNLKTLIKIGNWFTGTGFIAEMCLKI	623
Db	725	CITYVMDPVDLATAICIVLNTLFMAHEHPMTTEFNKVLAINGLVFTGTGFIAAEMVLK	784
QY	624	IADLPYHFRHGNNVPDSIVALLSLADVLYNTLSD-NNRSFLASURLVRVFKLAKSWPTL	682
Db	785	IAMPYEYOYGVGNIFDSLIVLSLVELF---LADVEGLSVLRSFERLLRVFKLAKSWPTL	841
QY	683	NTLIKIHSVGA LGNLTVVLTVVIFSVMGRULFGTKFNK-TAYATQERPRRRWHMDN	741
Db	842	NMLIKIIGNSVGA LGNLTVLVAIIFIFAVGMQLFGSKYECVCKINDCCTLPRWHMD	901
QY	742	FYHSELVVERILLGEWIENWCMODMGSLPICITIVFVLMVIGKLVVNLFIALLNSF	801
Db	902	FFHSELVFRVLGGEWIETFMWDCM- EVAGQAACLIVYMMVWVIGNLVNLFIALLLSUF	960
QY	802	SNEBKDGSGLEGETRKTKVOLADRFRRAFASFMLHALQSFCCCKRRKNPKPKETTETESA	861
Db	961	SSDNLT-AIEEDPDANNLQIATRICKGINVYKOTLREFILKAF-----SKPK-----	1008
QY	862	GENKDSILDPAPWKKEYDTDMALTYTGQACAPLAPAEVEDDEVCEYGE-----GALPTSQ	916
Db	1009	-----ISRREIROAEDLNTKENYISN-----HTLAEMSKGHNELKDKDISFGSGSVDK	1057

RESULT

RESULT
568453

S68453 sodium channel protein SNS - rat

Species: *Rattus norvegicus* (Norway rat)

C/species: Rattus norvegicus (Norway Rat)
C/Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text change 20-Jun-2000

C; Date: 17-JUL-1998
C; Accession: S68453

C; Accession: S68433
R; Akopian, A.N.; Sivilotti, L.; Wood, J.N.

Nature 379, 257-262, 1996

Nature 373, 237-242, 1995
 A; Title: A tetrodotoxin-resistant voltage-gated sodium channel expressed by sensory

A; Reference number: S68453; MUID: 96138382

A; Accession: S68453

A; Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-1957 <AKO>
A:Cross-references: GB:X92184; NID:g1209466; PIDN:CAA63095.1; PID:g1209467
A:Experimental source: gorsai root ganglia
C:Superfamily: sodium channel protein
C:Keywords: sodium channel; transmembrane protein; voltage-gated ion channel
F:132-148/Domain: transmembrane #status predicted <TM1>
F:158-174/Domain: transmembrane #status predicted <TM2>
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F:788-804/Domain: transmembrane #status predicted <TM9>
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Query Match 49.6%; Score 4545.5; DB 2; Length 1957;
Best Local Similarity 51.0%; Pred. No. 0;
Matches 966; Conservative 265; Mismatches 446; Indels 217; Gaps 36;

QY 15 NFRPFTSDSLAAIKRIAIQKERKSKDKAAAE-----PQRPOLDKASRLPKLYGDP 70
DB 12 NFRFTPSLEAEIEQIAHRAAKAKYKHRGQDEKGPQLDKDCNQLPKRYGELP 71

QY 71 PELVTKPLEDDPYVKDKHTFVNLNKRRTIYRFSAKRALFLILGPNPLRLSIRLSVHSV 130
DB 72 AELVGEPLDDPYFTSTHRTFVNLNKRRTISRSATWALWLFSPDNLRRRTAIVSVHSW 131

QY 131 FSMFTICVILNCFMANSMERSFNDIP---EYFVIGIYILEAVIKILARGFIVDEFSF 187
DB 132 FSIFITITILNVCVMTAT-----DLPEKVEYVFTYITFEALIKILARGFCLNEFTY 184

QY 188 LRDPNWLDLFIIGTAIATCPGSOVNL---SALTRFVRFAKIAISVISGLKVIIVGALL 244
DB 185 LRDPNWLDLFIIGTAIATCPGSOVNL---SALTRFVRFAKIAISVISGLKVIIVGALL 240

QY 245 RSVKLVDMVWLTFLCLSFALVGQOLFPMILNQKCIKNCGPNPASNKDCFEK----- 299
DB 241 HSVKRLADWTILTVCLSVFALVGLQFLKGNLKNKCIKNCGRNGTDPHKADNLSEMAEYIFIK 300

QY 300 KDSDFIMCGTWLGRPCPNGSTCDKTTLPNDNNTYKTDNFGWSFLAMFRVMTQDSWRL 359
DB 301 PGTIDPLLCGNSDAGHCPGGVCLKTPDNPFDNYTSPDSFAWFLSLFRMLTQDSWRL 360

QY 360 YRQILRTSGIVFVFVFVIFLGSPLNLLNLTLAVVTMAEYEQNNRVAAETAEKEMFOEA 419
DB 361 YQQTILASGKMYVFFVLVIFLGSPLNLLNLTLAVVTMAEYEQNNRVAAETAEKEMFOEA 420

QY 420 QLLREKEALVAMGIDRSSLSLNSQAASSFSP-----KKRFFGS----- 458
DB 421 LEVLQKEQVLEALGIDITSLQSHSGSPLASKNANERPVRKSRVSEGSTDDNRSQSDP 480

QY 459 ---KTRKSFMRGSKTAQASAD-----SEDDA----- 483
DB 481 YNORMSPLGLSGRRASRASHGVFHRAPSDISFPDGIPTDDGVFHGDQESRRGSILLG 540

QY 484 -----SKNP-----QLLEQTKRLSONLP-----VDL 504
DB 541 RGAGTGPLRSPPLPQSPNRRRGEQGLGVPTGELTAGAPALHTTQKSFLSAGY 600

QY 505 FDEHVDPLHRORALSAVSILITIQEQEKFOEPFCPCGNLASKYLVWDCSPQWLICKV 564

DB 601 LNE-----PRAQRAMSVSVMTSVIEELEESKLCPCCLISFAQKLYLIEWCCPKWRKFKMA 657
QY 565 LRTIMTDPTELAITICIIINTVFLAVEHHNMDLTKILKIGNVWFTGIFTAEMLCKII 624
DB 658 LFEVTDPAELTITLCIIVNTVFMABHPMTDAFQAMQAGNIVETVFTMEMAFKII 717
QY 625 ALDPYHYFRHGNVFDISVALLSLADVLYLNTLSDNNRFSLASLRLVLPFKLAKSWPTLNT 684
DB 718 APDPYHYFQKWNIFDCVITVTSLEL--SASKKGSLSVLRTLRLRLVFKLAKSWPTLNT 775
QY 685 LIKIIGHSVAGALNLTIVVIFSVVGMRLFGTKF--NKTAYATQERPRRRVHMDF 742
DB 776 LIKIIGSVGALNLTIFILAIIVFIFALVGKOLLEDCYCRKDGVSVMNGEKLRLHMDCF 835
QY 743 YHSFLVFRILCGEWIENMGMQMDGSPGLIIVFVILMVGKLVNLFALLNSFS 802
DB 836 FHSFLVFRILCGEWIENMGMQMDGSPGLIIVFVILMVGKLVNLFALLNSFS 894
QY 803 NE-----EKDGSLEGETRKTQVQLALDRFRFAFSFMLHALQSFCCCKCR-----RKNS 850
DB 895 ADNLTAPEDDGEV-----NNQLALARIQVILGHASRAIASIYISSHCRFHPKVTQIG 948
QY 851 PKPKETTESFAGENKDSILPDA-----RP-----WKEDYTDMLYTGQAGAPL 893
DB 949 MKPPLT-----SSEAKNHATDAVSAVGNLTYPALSSPKENHGDFITDENVW---VSVP 1001

QY 894 A-----PLAEVEDDVEYC-----GEGALPTSQHSAGVQAGDLPPETKQLTSPDD 938
DB 1002 AEGESDLDELEDEMEQASQSSWQEDPKGQOBOLPQVKCNHQHAARSP--ASMSSEDL 1059

QY 939 OGVEVEVSEEDHLHSIOSPKKSDAVSMSECSIDLND---IFRNLOKTVSPKKQDPR 995
DB 1060 APYLGESWRRKD---SQVPAEGVDDTSS--SEGSTVDCPDPEILRKIPELADDDLEPDD 1115

QY 996 CFPKLSGCHFLCHTKDRKSPVLMWNIRKTCYQVVKHSWFESFIIFVILLSGALIED 1055
DB 1116 CFTEGCTRRGCCNVNTSKSPWATGWKTCYRIHESWFESFIIFMILLSGALIED 1175

QY 1056 VNLSPRPOVEKLLRCDNIFTIFLLEMLKWAQGFRRYFTSACWCLDFLIVVSVLSL 1115
DB 1176 NYLEKPRVKSLEYLTDVFTFIFVEMLLKWAYGFKYFTNACWCLDFLIVVSVLSL 1235

QY 1116 M-----NLPSLKFRTLRALRPLRALSOPEGMKVVVVALISAPAILNVLVLCLEWL 1168
DB 1236 TAKILEYSDVASIKALRTRALRPLRALSRFEGMRVVDALVGLPISMNVLVLCLEWL 1295

QY 1169 VFCILGVNLFSGKFGRCINGTDINMY--LDTEVEPNRSCQNIEN---YSWKVPQVNFEN 1222
DB 1296 LFSIMGVNLFAGKFSKCYD--TRNPFNVNSTMVNNKSECHNQNSTGHFFVNVKVPFN 1354

QY 1223 VGNAYLALQVATYKGLWEIMNAAVDSREKDEQDPFANLAYLYFVFIIFGSPFTLNL 1282
DB 1355 VAMGYLALQVATYKGLWMDIMYAAVDSGEINSQPNWNNLYMYLYFVFIIFGSPFTLNL 1414

QY 1283 FIGVIIDNFNQOKKLGQDIFMTEEEKYNNAMKLGTKPKQKPIPLNKKQAFVPL 1342
DB 1415 FVGVIIDNFNQOKKLGQDIFMTEEEKYNNAMKLGSKPKQKPIPLNKNYQGFVEDI 1474

QY 1343 VTSQVDFVIIILGLIIVLNNIMMAESADQKDVKKFTDILNIAFVIFTECLIKVFAIRQ 1402
DB 1475 VTRQAFDIIIMVILCLNMTMMVETDEGEKTKVLGRINQFFVAVFTGECVKKFAIRQ 1534

QY 1403 HYFTNGWNLPCVVVVLSTLVSRL--LEDSDISFPPTLFRVVRILARIGRLRLVRAARG 1461
DB 1535 YYFTNGWNVDEFIVVILSIGSLFSAILKSLNENYSPTLFRVIRLARIGRLRLVRAARG 1594

QY 1462 IRTLLFALMMSLPISLFNIGLLLLFLVMFYIAFGMSWFSKVKGSIDIDIFNFTGSM 1521
DB 1595 IRTLLFALMMSLPALFNIGLLLLFLVMFYISFGMASFANVVDVDEAGIDDMFNKFTGSM 1654

QY 1522 CLFQITTSAGWDITLNPML--AKEHC-----NSSSDSCCOPOIATVYVYSYIIISFLI 1574
DB 1574 CLFQITTSAGWDITLNPML--AKEHC-----NSSSDSCCOPOIATVYVYSYIIISFLI 1574

Db 1655 CLFOITTSAGWDGLLSPILNTGPPYCDPNLPSNGSNGCNGSPAVGIIFFTYIIISFLI 1714
Qy 1575 VVNYIAVILENFATATEESDPLGEDDFELFYEVWEKFDPEASQFIQYSALSDFADALP 1634
Db 1715 VVNYIAVILENFVATEESTPELSEDDDFMFYETWEKFDPEATOFIAFSALSDFAADTLS 1774
Qy 1635 EPLRVAKPNKFOFLVMDLPVWYGBORLHCHMDVLFPAFTTRVYDSSGLDTMTKMTMEKMEEA 1694
Db 1775 GPLRIPKPNQILIQMDLPLVPGDKIHCLDILFAFTKNVLGESGELDSLKTNMEKFMAT 1834
Qy 1695 NPEFKLVEPIVTTTKREEEGOGAAVIOARXKHM 1728
Db 1835 NLSKASIEPIATLURWQEDLSATVIOAKRSYM 1868

RESULT 6

A46269
sodium channel alpha chain HBA - human

C:Species: Homo sapiens (man)

C:Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997

C:Accession: A46269

R:Almed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.

Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992

A:Title: Primary structure, chromosomal localization, and functional expression of a vol

A:Reference number: A46269; MUID:92390418

A:Accession: A46269

A:Molecule type: mRNA

A:Residues: 1-2005 <AHM>

A:Cross-references: GB:M94055

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIP:113082)

C:Genetics:

A:Map position: 2q23-q24.3

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match 49.18; Score 4501; DB 2; Length 2005;
Best Local Similarity 48.08; Pred. No. 0;
Matches 954; Conservative 284; Mismatches 449; Indels 300; Gaps 39;

Qy 11 PDERNFRPTSDSLAATKRTAIOK-----ERKSKDKAAAEPPQRPDLKASRLPK 64
Db 9 PGDPDSFRFTRESLAAEQRTAEAKRPQKERDEDD---ENGPKFNSDLEAGSLPF 64
Qy 65 LYGDIPPELVTKPLEDDPYKDKHTEMVNLNKRRTIVRFSAKRALFILGPNPLRSLMR 124
Db 65 IYGDIPPELVTKPLEDDPYKDKHTEMVNLNKRRTIVRFSAKRALFILGPNPLRSLMR 124
Qy 125 ISVHSVSMFICTVINCMPMANSMEKSFNDIPEYVIGIYILEAVIKILARGFVDE 184
Db 125 ILVHSLFNMLTMCILTNCVPMNSNPPDWTKNV-EYTFGTGIYFESLIKILARGFCLED 183
Qy 185 FSLRDPNNWLDLFIIGTATATCPGSOVNLALTRPVFRALKAKISVIGLKVIGALL 244
Db 184 FTLRDPNNWLDLFIIGTATATCPGSOVNLALTRPVFRALKAKISVIGLKVIGALL 242
Qy 245 RSVKRLVDVMTLFCLSIFALVGQOLPMGILNOKCIKHNGCPNPAS-----291
Db 243 QSVKRLVDVMTLFCLSIFALVGQOLPMGILNOKCIKHNGCPNPAS-----291
Qy 292 -----NKDCEFEKED-----SEDFIMCGTWLGRPCPGSTCDKTLNP 330
Db 301 DNGTGTENRTVSIFNWDIEKSHFYFLEGONDALLCGNSDAGQCPEGVICVAKGRNP 360
Qy 331 DNNYTKDFNCFWFLAMRVMTQSWERLYRQILRTSGIYVFFVVFVIFLGSYLLNLT 390
Db 361 NYGTSFDTFSWAFSLSLFRMLTQDFWENLYQLTLRAAGKTYMIFVLVIFLGSYLLNLT 420
Qy 391 LAVVTMAVEQNRNVAAETAEAKEMFQF-AOQLLREEKEALVAM-----GI 435
Db 421 LAVVMAVEQNRNVAAETAEAKEMFQF-AOQLLREEKEALVAM-----GI 430

QY 1205 QCNI--SNYSKVKPVQVNFNVGNAYLALLOVATYKGMLEIMNAAVDSREKDEQDPFEANL 1262
D 1334 DCQALGQARKKVNKVNFDNVGNAGYALLOVATEKGMWMDIMYAAVDSRDVKLQPIEENL 1393
QY 1263 YAYLVFVFIIFGFFFTLNLFIGVIIDNFNOQKRLGGODIFWTEBQKYYNAMKKLGTK 1322
D 1394 YMYLVFVFIIFGFFFTLNLFIGVIIDNFNOQKRLGGODIFWTEBQKYYNAMKKLGSK 1453
QY 1323 KQKPIRPLNKKCAFVLDVTSQVDFVILGLVLNMIIMAAVSADQPKDKVKTFTDILN 1382
D 1454 KQKPIRPAKFGQVDFVTVROVFDISIMILCLNKNVMTAVETDDQSKVMTLVLSRIN 1513
QY 1383 IAFVVFIEICLKVAFALROHYFTNGWNLFCVNVVVISIISTLVSL--EODSIDFPPTLF 1441
D 1514 LVFVLTGTGELLKLSLRYVYFTGNWIFDVFVVILSVGMFLAELIEKYFVS--PTLF 1571
QY 1442 RVVRLARIGRLRLVRAARGTIRTLFALMMLSLPSLFNIGLGLLFLVMYIYAFGMSWFSK 1501
D 1572 RVIRLARIGRLRLKAKGIRTLFALMMLSLPALFNIGLGLLFLVMYIYAFGMSWFSK 1631
QY 1502 KKGSGIDIFNFETFGSMCLFOITTSAGWDTLLNPMLEAKE-----HCNSSSDS 1553
D 1632 KKEAGIDMFNFETFGSMCLFOITTSAGWDTLLNPMLEAKE-----HCNSSSDS 1601
QY 1554 CQPOIAVVFVSVYIIISFLVNMVYIAVILENFNTATEESEDPLGEDDFEIFYEYWEKF 1613
D 1692 CGNPSVGIFVSVYIIISFLVNMVYIAVILENFNTATEESEDPLGEDDFEIFYEYWEKF 1751
QY 1614 DPEASQIYQVYALSDFADALPELRLVAKPNKQFLVMDLPMVMDRLHCHMDVLAFTTRV 1673
D 1752 DPDAQIIEFCVCLSDAAADPPLLIAPKNVQLIAMDPLMVSQDRHCLDILFAFTKRV 1811
QY 1674 LGDSGLDTMTKMEKFMKPKLYEPTVTTTKRKEEBOGAIVTORVKHMEKMYK 1733
D 1812 LGESGEMDALRIQWEDFMASNPVSVYEPITTLTKRKEEVSAAITQRYCY---LLK 1868
QY 1734 LRLKDRSS 1741
D 1869 ORLKNISS 1876
RESULT 8
A60054
sodium channel protein IIb, long form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C:Accession: A60054; B4824
R:John, R.H.; Moorman, J.R.; VanDongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster, Brain Res. Mol. Brain Res. 7, 105-113, 1990
A:Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in Xe
A:Reference number: A60054; MUID:90251117
A:Accession: A60054
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1983 <SOH>
R:Schaller, K.L.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A:Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A:Reference number: A4824; MUID:92211397
A:Accession: B4824
A:Molecule type: mRNA
A:Residues: 611-662 <SCH>
A:Cross-references: GB:597388; NID:q248225; PIDN:AAB21984.1; PID:q248226
A:Experimental source: skeletal muscle
A:Note: sequence inconsistent with the nucleotide translation
C:Note: sequence extracted from NCBI backbone (NCBIN:97388, NCBI:97391)
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane protein

Query Match

48.9%; Score 4489.5; DB 2; Length 1983;

Best Local Similarity 48.5%; Pred. No. 0;
Matches 951; Conservative 283; Mismatches 436; Indels 291; Gaps 38;
QY 11 PDENRNPFTSDSLAAIKRTAIAIKERKSKDK-AAAEQPPRPOLDLKASRLKPLKYGDI 69
D 9 GPSPFLRFTRESLAAIEKRAAEKAPKKEQDIDDENKPKNSDLEAGANLRFIYDI 68
QY 70 PPELVTPLELDPPYKDKHTFMVNLNKRRTIYRESAKRALFILGPFNPLRLMIRISVHS 129
D 69 PPEVSEPLELDPPYVSKTKTFVVLNKGKAIRESATSALVILPLNPKRIAIKILVHS 128
QY 130 VFSMFICTVIINCFMANSERSFDNDIPEYFIGIYILEAVIKILARGFIVDEFSLR 189
D 129 LFSMLIMCTIITNCFMFTLSNPPDMTKNV-EYTFGIYTFESLILKILARGCLEDFTLR 187
QY 190 DPWNLDFIVIGTATATCFPGSQVNLASALRTFRVRLKALISVIGLVKVIYGALLRSVKK 249
D 188 DPWNLDFIVIGTATATCFPGSQVNLASALRTFRVRLKALISVIGLVKVIYGALLRSVKK 246
QY 250 LVDVMTLFTCLSFALVQQLFNGILNKCICKHNCNPNASNKDCFEKEDS----- 302
D 247 LSDVMILTVFCLSVFALIGLQLEPMLNKLQW-----PPSD-SAPETNTTSYFNGTMD 300
QY 303 -----EDFIMCTWLGSRPCPNMGSTCDKTTLNPD 331
D 301 SNGTFVNVMTSTFNWKOYIADDSHFYVLDGQKPLLCGNGSDAGOCPEGYICVKAQRPN 360
QY 332 NNYTKDFNGFSGFLAMERVTQDSWERLYROILRTSGIYFVFFVWVIFLGSFYLLNLT 391
D 361 YGYTSEDTFSWAFUSLFLRMFTQDYWENDYQTLRAAGTKYMFVFLVIFLGSFYLVNLI 420
QY 392 AVVTMAYEEQNRAAETEAKEKMFQEAQALLREEKALVAN-----GT----- 435
D 421 AVVAMAYEEQNRAAETEAKEKMFQEAQALLREEKALVAN-----GT----- 435
QY 436 -----DR----- 437
D 481 LLESSEASKLSKSAKEWNRNRKRQRREHGNRADGDRFPKSESDSVKRRSFLLS 540
QY 438 -----SSLNSLOASSFSPPKRR-----KFFGSKT----- 460
D 541 LDGNPLTGDKKLCSPHOSLLSIRGSLFSPRNKSTISFSGRAKDVGESENFADDEHST 600
QY 461 -----RKSPFM-----RGSKTAQASAD-----SEDDAKSNPQLLBQ 493
D 601 FEDSESRDLSLVFPHRPPCERNNSVQASMSRVMVPLGPNANGKMHSTVDCNGVSLGTT 660
QY 494 -----KRLSQ-NLPVDLFDHVDPLHQRALSAVSILTTIQOEKQFQPCPCGKMLA 546
D 661 ETEVRKRLSSYQISMEMLE---DSSGQRAMSASILTNTMEELSESRQKPCPCWYRFA 717
QY 547 SKYLVWDCSPOMLCIKKVLRTIMTDPFTLAIITICIINTVFLAVEHNMMDNLTKLI 606
D 718 NVFLWDCDCLWLVKLVNLIWMDPFVLDLITICIVLTLFMAHEHPTMQTQSSVLTY 777
QY 607 GNVVFTGIFTAEMCLKIADLPYHFRHGMNVFDSIVALLSLADY-LYNTLSDNNRSLA 665
D 778 GNLVFTGIFTAEMVLKIIAMPDPIYFQBGWNIIDGIIIVLSLMEIGLANV--EGLSVLR 834
QY 666 SLRVLRFKLAQSVPTLNTLKIIGHSVGALGNLTIVVTIVVIFSVGMRLFGTKFNK- 724
D 835 SPRLRVFKLAKSWPTLNLKIIIGNSVGLNLTIVLAIIVFVAVVGMQLFGKSYKEC 894
QY 725 TAYATQERPRRRHMDNFYHSLFVFLVFTLCGEMENMWGMODDGSPLCIIVFLINVI 784
D 895 VCKINVOCKLPRHMDNFYHSLFVFLVFTLCGEMENMWGMODDGSPLCIIVFLINVI 784
QY 785 GKLVLNLFIALNLSFNSNEEKDGLSEGETRKTQVQLALDRFRRAFSFMLHALQSFCKK 844
D 954 GNLVLNLFIALNLSFNSNEEKDGLSEGETRKTQVQLALDRFRRAFSFMLHALQSFCKK 844
QY 845 CRRK---NSPKPKETTESFAGENKDSILPDARPKWEYTDMLYTGQAGAPLAEVIED 901
D 845 CRRK---NSPKPKETTESFAGENKDSILPDARPKWEYTDMLYTGQAGAPLAEVIED 901

Db 1008 CFRKAFFRKPVKVIEIQEG-----NKIDSCMSNNTG-----IEISK 1042
Qy 902 DVEYCGEGALPTSQHSAGVQAGD-----LPPETKQLTSP-----DDQG 940
Db 1043 ELNYLKDNGT-----TSGVGTGSVEKYIVDENDYMSFINPSLTVTVPIAVGESDPEN 1097
Qy 941 VEMEVSFEDLHLSIQSRKSDAVSMLSEGTDLNIDFRNLQKTVSPKK--QPDRCFF 998
Db 1098 LNTFEFSSES---ELEESKELNATSS--SEGSTDVAPPREGEQAEIEPEDLKPACT 1153
Qy 999 KGLSCHFLCHTKDRKSPWLWNNIRKTCYOIVKHSWFESFIIFVILLSSGALIFEDVNL 1058
Db 1154 EGCIKKFFQCVSTBEGRKGIWNLRLKTCYSIVEHNWPETETIVFMILLSSGALAFEDIYI 1213
Qy 1059 PSRQVEKLLACTONIFITFELLEMILKWAFGRPRYTSACWLDLFLIVVSVLSLM-- 1116
Db 1214 EORTKTKMVEYADKVFTYIFILEMLLKWAVGQTYFTNAWCWLDLFLIVDVSVLSVAN 1273
Qy 1117 -----NLPSLKSFRLLRALRPLRALSQEGMKVYVYALISAIPALNVLVCLIFWLVC 1171
Db 1274 ALGYSELGAIKSLRFLRALRPLRALSREGMRVNVNALVGAIPSMNVLLVCLIFWLIFS 1333
Qy 1172 ILGVNLFSGKGRGCIINGTDINWLDTEVPNRSCNI---SNYSWKVPQVNDNNGNAYLA 1229
Db 1334 IMGVNLFAKGFYHCVNTTGNMF-EIKEVNNFSDCQALGKQARKNVKVNFDNNGAGYLA 1392
Qy 1230 LLOVATYKGLFEMNAADVSRKEDQDPDFEANLAYLYFVVFIFGSEFTLNLFVGIID 1289
Db 1393 LQOVATFGWMDIMVAAVDSRDVKLQPIYEENLYMVFVIFIFGSEFTLNLFVGIID 1452
Qy 1290 NFNOQKRLGGQDIFMTEEQKYYNAMKLGTKPKQKIPRPLNKKQAFVDFLVTQVFD 1349
Db 1453 NFNOQKRLGGQDIFMTEEQKYYNAMKLGSKPKQKIPRANKFQGMVDFVTRQVFD 1512
Qy 1350 VIILGLVNLIMMAESADQPKVKKTFDILNTAFVVFIFTECLIKVFALRQHYFTNCW 1409
Db 1513 ISIMILICLNMVTMVEVDQSKYMTLVLSRLNLFVILFTGEFLKLKLSLRYVFTIGW 1572
Qy 1410 NLFQCVVVLSTISLTVLSRL-EDSDISFPPTLFRVVRRLRIGRILLYRAARGITLLFA 1468
Db 1573 NIFDFVWVLSVIGVFLAELEKIEFVS--PTLFRVIRLARIGRILRLIKGAGINTLLFA 1630
Qy 1469 LMMSLPSLNFGLLFLVWFYIAYFGMSWFSKVRKGGSIDIDIFNPETFTGSMCLFQITTT 1528
Db 1631 LMMSLPALFNGLLFLVWFYIAYFGMSNFAVYKKEAGIDDMFNFTPGNSMCLFQITTT 1690
Qy 1529 SAGWDTLNLPMLEAKE-----HCNSSQSDSCQOQIAYVYFVSYIIISFLIVVNNYI 1580
Db 1691 SAGWDGLLAPILNSAPPDPCDPAIHGSSVRKGDGCPNSVGIFVFVSYIIISFLIVVNNYI 1750
Qy 1581 AVILENFNTATEESDPLGEDDFEIFYEWEKFDPEASQFTQYSALSDFADALPEPLRVA 1640
Db 1751 AVILENFVATEESAEPDSEDDEFYEVWEKFDPDATQFTEFKLSDFAAALDPPPLLIA 1810
Qy 1641 KPNKQFLVMDLPMVNGDRLHCDMVLFAFTRVLGSDGLDTMTKMTMEKEKFEANPEKKL 1700
Db 1811 KPNKQFLVMDLPMVNGDRIHCLDILFAFTRVKGESGEMDALRLOMEDRWASNPFSKVS 1870
Qy 1701 YEPVITTTKRKEEGOGAAVIOARVKKHMKVUKLKDORS 1741
Db 1871 YEPITTTLLKRQEEVSAIIQNRVRY---LLKQRLKNISS 1908

RESULT 9

B25019 sodium channel protein II - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999

C:Accession: B25019; S24804

R:Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.

Nature 320, 188-192, 1986

A:Title: Existence of distinct sodium channel messenger RNAs in rat brain.

A:Reference number: A93377; MUID:86146901

A:Accession: B25019
A:Molecule type: mRNA
A:Residues: 1-2005 <ND>
A:Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A:Description: Developmentally regulated RNA splicing of rat brain sodium channel mr
A:Reference number: S24803
A:Accession: S24804
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 183-188, 'D', 190-305 <SAR>
A:Cross-references: EMBL:X61149; NID:g57074; PIDN:CAA43458.1; PID:g57076
C:Superfamily: sodium channel protein
C:Keywords: duplication; ion transport; sodium channel; transmembrane protein; volta

Query Match 48.9% Score 4484.5; DB 2; Length 2005;
Best Local Similarity 48.1% Pred. No. 0;
Matches 950; Conservative 278; Mismatches 448; Indels 301; Gaps 38;

Qy 11 PDERNRPFTSDSLAAIKKRIAOK-----ERKSKDKAAAEPOPRLQDLKASRKLPK 64
Db 9 PGDSFRFTRESLAAIEORIAEBKAKRPQKERKEDD-----ENGPKPNSDLEAGKSLPF 64
Qy 65 LYGDIPPELVTKPLEDDPYKDKHKTVMVANKRTIYFSAKRALFILGPENPLRSLMR 124
Db 65 IYGDIPPELVTKPLEDDPYKDKHKTIVLANKRAISFATSALYILTPFPNIRKKAIR 124
Qy 125 ISVHSFMSFTICTVIIINCMFMANSMERSFNDIPEYVFIGIYILEAVIKILARGFIVDE 184
Db 125 ILVHSLFNVLMICILITNCVFMTKSNPPDWTKNV-EYFTGTGIYTFESLIKILARGFCLE 183
Qy 185 FSLRDPNWLDFIVIGTAIATCFPGSOVNLISALRTFRVFRALKAISVIGLKVIYVALL 244
Db 184 FTELRLPNWLDFTVITPAYVTEFV-NLGNVSALRTFRVLRALKTISVIGLKTIVGALI 242
Qy 245 RSVKKLVDVWVLTFLCISIFALVGOOLPMGLILNKKCIKHNGCPNPASN----- 292
Db 243 QSVKRLSDVMLTIVFCLSVFALIGLQFLNLRNKLQW-----PPDNRSTFINTSFTN 297
Qy 293 -----KDCFEKEKDESEIDIMCGTWLGSRPCPNCGSCDKTT 327
Db 298 NSLDNGWTFAPNRTVNMFMNWEYIEDKSHFYFLEGONDALLCGNSSDAGCQPGYICVRAG 357
Qy 328 LNPNNYTKFNFNGSFLAMFRVMTQDSWERYLROIILRTSGIYFVFFVWVIFLGSFYLL 387
Db 358 RNPNGYTSFDTFSWAFSLFLRLMTQDFWENLYQLTLRAAGKTYMIFFLVIFLGSFYLI 417
Qy 388 NLTAIVVTMAYEEQNRVAAETAEKEMFOE-AQOLLREEKEALVAM----- 433
Db 418 NLILAIVAMAYEEQNQATLEAEQKEAEFOMLKQKQBEAQAAAAAASRDSFGA 477
Qy 434 -GIDRSSLSNQASFSFSPKPKKFFGSKTRK----- 462
Db 478 GGIGVFSESSVASKLSSKEKELKNRKKKKQKEQEEBEKEDAVRKSASEDSIRKKG 537
Qy 463 SFFMRGSKTAQ----- 482
Db 538 QFSLGSRLLTYEKRFSPHQSLLSIRGSLSPRRNSRASLNFNFKGRVKDIGINSENDAD 597
Qy 483 -----ASKNPQLLEOTKRLSONLPV----- 502
Db 598 HSTEDNDSRDSLVFPHRHGERRPSNVQSASRASRGITPLPMNGKMHSAVDCNGVSVSLV 657
Qy 503 -----DLFDE-----HV-----DPLHRQRALSVAISILITIQ 529
Db 658 GGPSALTSVPQQLLEPGTTTETETIKRRSSSYHVSMDDLEDP-SRQRAMSMASILNTME 716
Qy 530 EOEKQEPCEPCGKNLASKYLVWDCSPWLICIKVLRITMTDPPTELAITICIIINTVFL 589
Db 717 ELESROKCPCKWKFKANMCLIMWCKPKLVKHVNVLVMDPPFDLAIITICIVLNTLFM 776

Qy 590 AVEHNNDNKTILKIGNWVTGIFIAEMCLKIITADLPYHYFRHGNVWFDSIVALLSLA 649
Db 777 AHEHPMTQEFSVGNLVNFTGFTAEMLFKIITAMPYVYFQGWNIIDGFIYLSLSL 836
Qy 650 DV-LYNTLSNDRSPLASIRVLRFKLAWSPTLNTLKIIGHSVGALGNLTIVLTVFV 708
Db 837 ELGLANV---EGLSVLRFRLLRVFKLAWSPTLNTLKIIGHSVGALGNLTIVLTVF 893
Qy 709 IFSVGMRLFGTKFNKTAYATQ---ERPRRRWHMDNFYHSFLVFRILCGEWIENMWGM 765
Db 894 IFAYVGMQLFGSKYKCYCKISNDCLEP--RHHMHDFEHSFLVFRILCGEWIENMWGM 951
Qy 766 QMDGSPICIIIVIMVIGKLVNLFIALNLSFNEEKDGLSEGTTRKTKVOLALDR 825
Db 952 -EVAGTMCITVFMVMVYIGNLVNLFIALNLSFSSDNL-AAADDNEMNNLQIAVGR 1009
Qy 826 FRAFSFEMHALOSPCKCKRKNSP---KPKETTESFAGENKDSILDPARPNKEYDTD 881
Db 1010 MOKGIDFVKRIRFQAFVKQKALDEIKPLEDLNN---KKDSCISN----- 1055
Qy 882 MALVTGAGAPLAPLAIVEDDVEYCGEG---GALPTSHSAGVQAGD---LPPETKQL 933
Db 1056 -----HTTIEIGKDLNLYLKDCNGITTSIGSSVEKYVYVDESVMFINNPSLTV 1103
Qy 934 TSP-----DQGVEMEVSEEDLHLSQSPRKSDAVMSLSECTIDLNDIFRLQKTV 987
Db 1104 TVPIALGESDFENLNTFESSSES-----DMEESKEKLNATSS-SEGSTVDIGAPAEQPEA 1159
Qy 988 SPKK--OPDRCPKGLSCHFLCHTKDRKSPVLMWNNIRKTCYQIVKHSWESFIIFVIL 1045
Db 1160 EPESELEPEACTEDCVKRFKCCQISIEEGKGLMNNIRKTCYKIVENHWFETTFVFMIL 1219
Qy 1046 LSSGALIFENLPSRPOVEKLRCTDNIFTIFILEMLKWAFAFRFRYFTSAMCWLDF 1105
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Qy 1106 LIVVSVLSL-----MNLPSLKSFRTRLRALRPLRALSQEGMKVYVALISATPALN 1158
Db 1280 LIVDVSLSLTANALGYSELGAIKSLRTRALRPLRALSREGMVYVVALIGALPSIMN 1339
Qy 1159 VLLVCLIFWLVFCILGVNLFSGKFCRCINGTDINNLYDFTVPRNSQCN---SNYS--W 1213
Db 1340 VLLVCLIFWLVFIMGVNLFAGKFYHCINYYTGEMF-DVSVVNNYSECOALIESNQTA 1398
Qy 1214 KVPQNFNDVNGYALLQVATYKGLWLEIMNAADVSREKDEQDPEANLYAYLYEWFVFI 1273
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Db 1519 KQGMVFDVTKQVDFISIMILICUNMVTMMVETDQSQEMTNILYNLNFVILFTGEC 1578
Qy 1394 LIKVPALQHYFTNGWNLFDVNVVLSIISLTLSRL-BDSDISPPPTLFRVVRRLARIGRI 1452
Db 1579 VLKLSLRHYFTGNWIDFVNVVLSIVGFLAELEIKYFVS--PTLFRVRLARIGRI 1636
Qy 1453 LRLVRAARGIRTLFPALMNSLPSFNIGILLFLVNFYIAFGMSWFSKVKSGGIDIDFN 1512
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Qy 1513 FETFGSMCLFQITTSAGWDTLLNPMLEA-----KEHCNSSQSCQOQPIAVYVF 1564
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Qy 1565 VSYIIISFLVNMVYIAVILENFNTATESEDPGLGEDDFEIFYEYWEKFDPEASQFIQYS 1624
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Qy 1685 TMMEKEKFEANPPFKLYEPIVTTTKRKEEEOGAAVIOARAYRKHMEKMKVLRKLDSS 1741
Db 1877 IOMERFMAWSPSKVSYEPITTTTLARKQOEVSATVIOAIRRY---LLQKQVKVYSS 1930
RESULT 10
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A:25019
Sodium channel protein I - rat
N:Alternate names: sodium channel protein A
C:Species: Rattus norvegicus (Norway rat)
G:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C:Accession: A25019; S40783; I84764
R:Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.
Nature 320, 188-192, 1986
A:Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A:Reference number: A93377; MUID:86146901
A:Accession: A25019
A:Molecule type: mRNA
A:Residues: 1-2009 <NOD>
A:Cross-references: GB:X03638; NID:g57216; PIDN:CAA27286.1; PID:g57217
A:Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A:Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel.
A:Reference number: S40782; MUID:92051314
A:Accession: S40783
A:Molecule type: DNA
A:Residues: 177-253 <SAR>
R:Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A:Title: Structure and function of sodium channel.
A:Reference number: I50536; MUID:87311395
A:Accession: I84764
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2009 <RES>
A:Cross-references: GB:M22253; NID:g1041088; PIDN:AAA79965.1; PID:g1041089
C:Superfamily: sodium channel protein
C:Keywords: duplication; ion transport; sodium channel; transmembrane protein; volta

Query Match 48.8% Score 4476; DB 2; Length 2009;
Best Local Similarity 47.9% Pred No. 0;
Matches 942; Conservative 289; Mismatches 444; Indels 292; Gaps 39;

Qy 11 PDERNFRPTSDSLAAIKKRIAIQERKKSKDKA-AAEPQPRPOLDKASRKLPKLYGDI 69
Db 11 PDSFNF--FTRESLAAIERIAEAKKPNKPKDKDDENGPKPNSDLEAGKNLPFIYGI 68
Qy 70 PPELVTKPLEDLDPYIKDHKTFMWLNKRTYRFSAKRALFILGPNPLRSLMIRSVHS 129
Db 69 PPEMVSEPLEDLDPYIINKTFIVLNKKAIFRSATSALYILTFNPLRKIAIKILVHS 128
Qy 130 VFSMFIICTVIINCVMANSMERSFDNDIPEVVFVIGVILEAVIKILARGFTVDSFSLR 189
Db 129 LFSMLIMCTILNCFVMTMSNPDPWTKNV-EYTFGTFTFESLIIKIIARGFCLDEFTPLR 187
Qy 130 DPWNMLDFTVIGTATATCFPGSQVNSALRTPFRFRALKAIISVIGLVKIVGALLRSVKK 249
Db 188 DPWNMLDFTVITFAVYTFEV-DLGNVSALRTPFRVRLAKTISVIGLKTIVGALIOSVKK 246
Qy 250 LVDMVNLTLFCLISIFALVQQLFMGLINQKCI-----KHNGGNPNAS-----N 292
Db 247 LSDVMILVFCVLSFVALLGLQFLMGLNRKNCVQWPTNASLEHSEKNTVDYNGTLVN 306
Qy 293 KDCFPEK-----KDE-----DFIMCGTWLSRCPNCGSTCDKTTLNPNNTKPD 338
Db 307 ETVFEDFKSKYIQDSRYHYFLLEGVLDALLCGNSSDAGOCPEGYMCVACGRNNGYTSFD 366
Qy 339 NFGWSFLAMFRVMTQDSWRLYRQILRTSGIYFVFVVVIFLGSFYLLNLTAVVTMAY 398

Db 367 TFSWAFSLFRLMTODFENLYQLTLRAAGTKYIMFFVLVFLGSLYLINLILAVAMAY 426
QY 399 EEONRNVAATEAKEMFOEQAOQLLREEKEAL-----VANGIDRSSLNS 442
Db 427 EEONQATLEEAQKAEFOQMLEQKQOEAAQAAAAATASEHSREPSAAGRLSDSSSEA 486
QY 443 LQASSFSFKRK-----PFGSKT-----RKSEFM----- 466
Db 487 SKLSKSAKERNRRKKRQKQESGGEKDDDFHKSESDSIRKGRFSGIEGNRLTYE 546
QY 467 -----RGSKT-----AQASASDESDASKNP 487
Db 547 KRYSSPHQSLLSIRGSLSPRRNSRTSLFSFRGRAKDVSENFADDEHSTFEDNESRRD 606
QY 488 QL-----LEOTKRLS-----Q 498
Db 607 SLFVPRRGERRNSLSQTSRSLRMLAGLPANGKMHSTVDCNGVYVVGSPVTPSPVQ 666
QY 499 NLPVDLDFE-----HV-----DPLHROALSAVSILITITIOE 530
Db 667 LLPEVIDKPADTONGTTTETEMKRKRSSSFHVSMDFLEDFSQRORAMSIASILNTVEE 726
QY 531 QEKFOEPCPCCKNLASLYWDCSPQWLCIKKVLRTIMTDPFTELATITICIIINTVFLA 590
Db 727 LEESRQKPCPCWKYFSLFWDGSPYWLKVKHIVLVVMDPFVDLAITICIVLNTLEMA 786
QY 591 VEHHNMDDNLTKLIGWNVGTGFIABMKLITALDYPHYFRGWNVFDSIVALLSLAD 650
Db 787 MEHYPMTEHFNHVLTVGVNLTGFIPTAEMFLKIIITAMDPIYFYFQEGNIFDGFIVTSLVE 846
QY 651 V-LYNTLSDNNRSLASLVRVFKLAKSWPTLNTLKIIGHSVGCALGNLWTLTVVFI 709
Db 847 LGLANV---EGLSVLRSEFLRLRVFKLAKSWPTLNLNLIKIIGSVGCALGNLWTLTVVFI 903
QY 710 FSVGMRLFGTKFNKTA--YATQ--ERPRRRWHMDNFYHFLVFRILCGEWNENMGCMQ 766
Db 904 FAVVGMQLFGKSYKDCVKIATDCKLP--RWEMDNDFHFSFLVFRVLCGEWETWDMCM- 960
QY 767 DMDGSPCLIIIVLVWIKLVNLFTALLNFSNEEKDGSLEGETRKYKVLQALDRF 826
Db 961 EVAGQAMCLTVFMVMVVRNLVNLFLALLLSFSADNL--AATDDDDNEMNLQIAVDRM 1019
QY 827 RRAFSEMLHALQSFCKCKRKNPKPKETTESFAGENKDSILDPARWKEY----DTDM 882
Db 1020 HKGVAYYKRIYEF-----IQSFV--RKQILDEIKPLDNLNRKDNC 1062
QY 883 ALYTGQAGAPLAPAEVDDVEYCEGAGL-----PTSQHSAGVQAGDL 926
Db 1063 SNHTTEIGKLDCLKDVNGTSGIGTSSVEKYIIDESDYMSFINNPSTVTVPIAVGE- 1121
QY 927 PPETKQLTSPDQGVEMEVSEEDLHLSIQSPRKSDAVSMLSECTSIDLNDIFRNLOKT 986
Db 1122 -----SDFENLNTDFSES-----DLESSEKLNSSSSSGSTVDIGAPAE-OPV 1168
QY 987 VSPKK--OPDRCPFKGLSCHFKTKRKPWVLWNNIRKTCYQIVKHSWFESFIIFVI 1044
Db 1169 MEPEETLEPEACFTGCVQRFKCCQISVEEGRGKQWNLRTCFRIVEHNNFETFIIVMI 1228
QY 1045 LLSSGALIFDVNLPSPRQVEKRLRCTDNIETFIPLLEMLKWWAFGRFRRTYSAMCWL 1104
Db 1229 LLSSGALAFEDIYIDORKTIKTMLEYADKVFTYIFILEMLLKWVAYGYQTYFTNACWL 1288
QY 1105 FLIVVWSVLSL-----MNLPSLKSFRTLRALPLRALSQFEGMKVVVVALISAIIPAIL 1157
Db 1289 FLIVDVSLSVTANALYSSELGALKSLKTLRALPLRALSFEGRVVRVVALIGAIPSI 1348
QY 1158 NVLLVCLIFLWVFCILGNLFSGRFGRCINGTDINMYLDFTEVPNRQOC-----NISNYS 1212
Db 1349 NVLLVCLIFLWVFSIMGNLFAGRFYHCVNTTTGDTF--EITEVNNHSDCLKLIERNETAR 1407
QY 1213 WKVPQVNDVGNVAYLALLQVATYKGLWEIMNAAVDSREKDEQDPDEANLYAYLYFVVFI 1272
|| :||||| ||:|||||:||||| : || :||:|||||:|||||:||||| |||

Db 1408 WKNVKNVFDNMGFGYLSLLQVATEKGMWDIMVAAVDSRNVLEQPKYEESSLYMYLVFVFI 1467
QY 1273 IFGSFPTLNLFGIYIIDNPNQOKKLGQDIPMTIEQKYYNAMKKLGTKKPKQKIPRPL 1332
Db 1468 IFGSFPTLNLFGIYIIDNPNQOKKKGQDIPMTIEQKYYNAMKKLGTKKPKQKIPRPG 1527
QY 1333 NKCOAFVFDLVTSOVDVILGLVLNMIIMMAESADOPKDKVTFDILNIAFVVFITJE 1392
Db 1528 NKFGMVDFVTRQVDFISIMILICLNMVMMVETDDQSDYVTSLSRLNLFVIFVTGE 1587
QY 1393 CLIKVFALRQHYFTNGWNLFDVCVVVLSIISLVSRL--EDSDISPPPTLFRVRLARIGR 1451
Db 1588 CVLKLSURHYFTTGMNIFDFVVVLSIVGMFLAEELIEKYPVS--PTLFRVRLARIGR 1645
QY 1452 ILRLVRAARGIRTLFALMMSLPSLFNIGLLLFVWFIYAFGMSWFSKVKKSGSIDDI 1511
Db 1646 ILRLIKAGKIRTLFALMMSLPALEFNLGLLLFLVWFIYAFGMSWFSKVKKSGSIDDI 1705
QY 1512 NFETFTGSMCLFQITTSAGWDTLLNPMLEAK--EHCN-----SSSDSCQOPOIAVY 1563
Db 1706 NFETFTGSMCLFQITTSAGWDTLLNPMLEAK--EHCN-----SSSDSCQOPOIAVY 1563
QY 1564 FVSIIISFLVNMVIAVILENENFTESEDEPLGEDDFEIFYEWEKFDPEASQFIQY 1623
Db 1766 FVSIIISFLVNMVIAVILENENFTESEDEPLGEDDFEIFYEWEKFDPEASQFIQY 1623
QY 1624 SALSDFADALPEPLRVAKPNKFQFLVMDLPVWMDRLHMDLVFAFTTRVLGDSGLDTM 1683
Db 1826 EKLQSOFAALPEPLRVAKPNKFQFLVMDLPVWMDRLHMDLVFAFTTRVLGDSGLDTM 1683
QY 1684 KTMKEKPMKANPKKLYEPIVTTTKRKEEBOGAIVQIARVYRKHKMEK 1730
Db 1886 RQMEERPMASNPSPKSVQPTITTLKRQKEVSAVIOIARVRRHLK 1932
RESULT 11
CHRTM1
sodium channel protein mul alpha chain, skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 22-Jun-1999
C:Accession: JN0007
R:Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.;
Neuron 3, 33-49, 1989
A:Title: Primary structure and functional expression of a mammalian skeletal muscle
A:Reference number: JN0007; MUID:90148778
A:Accession: JN0007
A:Molecule type: mRNA
A:Residues: 1-1840 <TRI>
A:Cross-references: DB:M26643; NID:g205651; PIDN:AAA41682.1; PID:g205652
C:Comment: Action potentials propagated by skeletal muscle sodium channels are respon-
C:Comment: This heavily glycosylated protein contains four homologous domains, each
C:Comment: This protein is distinct from but related to sodium channel proteins isol-
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phospho-
F:120-458,561-813,1013-1305,1335-1611/Region: duplication
F:56,251,1321,1504/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase)
F:214,288,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site:
Query Match 47.6%; Score 4363.5; DB 1; Length 1840;
Best Local Similarity 49.3%; Pred. No. 2.8e-316;
Matches 908; Conservative 275; Mismatches 427; Indels 233; Gaps 35;
QY 11 PDENFRFTSDSLAAIKKRIATQKCK--KSKDKAAAEQPRPOLDLKASKRLPKLYGD 68
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QY 69 IPPELVTKPLDLDPPYKDKHTFMVNLKRTIYFSAKRALFILGPFNPLSLMTRISVH 128
Db 71 PPPEVIGTPELDDPPYSDKKTFFVLNKGKALFRSATPALYLSPPFSIVRVAIKLIH 130
QY 129 SVFSMFICTVIINCMEFMANSMERSFNDPIPEYVFIGIYILEAVIKILARGFVDFEFL 188
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Db 131 ALPSNFMITILLNCVMTWNSPPSWKSHV-EYTFGTGIYTFESLIKMLARQFCIDDTFEL 189
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Db 190 RDPNWLDFSVITWAYVTEF-DLGNISALRTRFRVRAKKAISVISGKIVTGALLRSVK 248
Qy 249 KLVDVWVLTFLCLISFALVGOQLPMGLINOKICKHNGCPNPASN----- 292
Db 249 KLSVDMILTFLCLISFALVGOQLPMGLINOKICKHNGCPNPASN----- 305
Qy 293 -----KOCFEKE-----KDSDEFMCGTGLSGRCPN 319
Db 306 WYGNWTWYINDTWNSQSWAGNSTFDWEAYINDEGNFYFLEGSNDALLCGNSSDAGHCP 365
Qy 320 GSTCDKTLTPNDNNYTKDFNGSFLAMFRVMTQDSWERYLRQLRTSGIYFVFVVVVI 379
Db 366 GYECIKAGRPNYCYTSDYTFSWAFALFLRLMTQDYENLFLQLTRAAGTKYMIFFVVII 425
Qy 380 FLGSFYLLNLTLAVVTWAYEBOQRNVAATEAKEMFOEAQQLLREBEKALVANGIDRSS 439
Db 426 FLGSFYLLNLTLAVVTWAYEBOQRNVAATEAKEMFOEAQQLLREBEKALVANGIDRSS 476
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Db 503 GSLDASGEKGP-----RFSQSADSASIDAMEEAEHAKQCPWPKYKCAHKVLIWNCAPW 559
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Qy 938 DOGVEMEVSE-EDLHLSIQSPRKSDAVSMLSECSITIDLIDNFRNLQKTV--SPK-KQP 993
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Qy 1343 VTSQVDFVILGLLIVLNMIIMASADQPKDKVTKTFDIL---NTAFVVIIFTIECLIKVFA 1399
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Qy 1400 LRQHYFTNGWNLFDVGVVLSIISLVSRLSEDSISFPPTLFRVVRRLARIGRLRLVRAA 1459
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Db 1459 KGIRTLFALMMSLPSEFNIGLILFLVMFIYAFGMSWFSKVKGGSGIDIDFNPFETFGS 1518
Qy 1520 MLCLFOITTSAGWDTLNLMLEA-----KEHCNSSSDSCQOQPIAVVYFVSYIIS 1571
Db 1519 IICLFEITTSAGWDTLNLMLEA-----KEHCNSSSDSCQOQPIAVVYFVSYIIS 1578
Qy 1572 FLIVVNYIAVLENFNTATESEDPGLCEDDFEIFYEWEKFDPEASOFIQYSALSDFAD 1631
Db 1579 FLIVVNYIAVLENFNTATESEDPGLCEDDFEIFYEWEKFDPEASOFIQYSALSDFAD 1638
Qy 1632 ALPPLRVRKPKFQFLVMDLPMVMGDRLHGMVLFATFTTVLGSSGLDGMTKMEKRF 1691
Db 1639 TLQEPKTKAKPNKIKLITDLPMVPGDKIHCLDILFALTKEVLGSGGMDALKQTMERKF 1698
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I64893
sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999
C:Accession: I64893
R:George, A.L.
Ann. Neurol. 31, 131-137, 1992
A:Title: Primary structure of the adult human skeletal muscle voltage-dependent sodi
A:Reference number: 151964; MUID:92246457
A:Accession: I64893
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1836 <RES>
A:Cross-references: GB:M81758; NID:g338212; PIDN:AAA60554.1; PID:g338213
C:Genetics:
A:Gene: Skm1
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 47.5%; Score 4355.5; DB 2; Length 1836;
Best Local Similarity 49.3%; Pred. No. 1.1e-315;
Matches 908; Conservative 271; Mismatches 415; Indels 249; Gaps 35;

Qy 17 RPTFSDSLAAIKKRIAIQKERR--KSKDKAAAAEPQRPQOLDLKASKRKLKLYGDPPELV 74
Db 18 RPTFSDSLAAIQEOR-AVEEARLQKQKQMEIEEPKPRSDLEAGKLNPLMYGDPPELV 76
Qy 75 TKPLEDDLPYKDHKTFWLNKRTIYRFSAKRALFILGPNPLRSLMIRISVHVSFMF 134

Db 77 GIPLEDLPYYNKKTFIVLNKRAIPRESATPALYLSPESVVRGAIKVLIIHALPSMF 136
QY 135 IICVILINCMPANMERSFNDIPDYVFIGIYILEAVIKILANGFIVDESFLRDPNNW 194
Db 137 IMITILNCVPMFMSDPPWSKNY-EXTFTGYTFESLIKILANGFCVDDFTFLRDPNNW 195
QY 195 LDFVIGTAICTCPGSONLSALRTPRVFRALKAISVISGLVKVIVGALLRSVKKLVDVM 254
Db 196 LDFSVMWAYUTEV-DLGNISALRTPRVLRALKTIIVIPGLKTIIVGALIOSVAKLSLDM 254
QY 255 VLTFLCLISFALVGOQLFMGLINOKICKHNCNPNAS- 292
Db 255 ILTVECLSVFALVGLQFMGLNRQKVR--WPPFENDNTTWYSNDTWYGNEM 311
QY 293 -----KDFEKB----- 311
Db 312 WYGNDSWYANDTWSHASWATNDTFDWDAYISDEGNFYFLGSDNALLCGNSDAGHCPK 371
QY 320 GSTCDKTTLPDNNYTKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIVFVFVVV 379
Db 372 GYECIKTRGNPNYGYSDTFSWAFALFRMLTQDYWHENLEQLTLRAAGKTYMIFVVII 431
QY 380 FLGSYLLNLPLAVTWAYEQNRNVAETAKEKMFQEAQOLLREEKEALVAMGIDRSS 439
Db 432 FLGSYLLNLPLAVVAMAYABQNEATLAEDKEKEEFOQMLEKTKKHQEL----- 482
QY 440 LNSLOASFSFKKRFSGSKTRKSFMRGSKTAQA---SASDEDDASKNPOLLEQTKRL 496
Db 483 -----EKAQAQALEGGEADGDPHAGKDCNGSLDTSQ 515
QY 497 SQNLPLVDFBHVPLHRQRALSASVILITIQOEKFOEPCFCGNLASKYLVDWCSP 556
Db 516 EKGA-----RQSGSDSGISDAMEELEEAHQKCPWYKCAKVLWDCCA 562
QY 557 QWLCKIKVLRITMDPTTELATITCIINTVFLAVEHHNMDNLKTLKIGNWFTGIFI 616
Db 563 PWLFKNIILHIVMDPPFDLTICIVLTLFMAMEHYPMTEHFDNVLTVGNLVTGIFT 622
QY 617 AEMCLKIILADPYHFRHGNVFDISIVALLSLADY-LYNTLSNNRSLASLRLVLPFKL 675
Db 623 AEMVCLKIAMPDYFOOGNWFISIIIVTSLVELGLANV---OQLSVLSRFLRLVLPFKL 679
QY 676 AKSWPTLNLKIKIIGHSGALGNLTIVLTIVVFISVVGMLFGTKFNK-TAYATQERPR 734
Db 680 AKSWPTLNLKIKIIGNSVAGLGNLTIVLAIIVFIFAVVGMQLFGSKYKCYCKALDCNL 739
QY 735 RRWMDNPFSLVFRILCGEWIENMMGQMDGSPLCIIVFVLIMVIGKVLVNLFI 794
Db 740 PRWHMDFFHSLFVFRILCGEWIETWMDCH-EVAGQAMCLTVFLMVVIGNLVVLNLF 798
QY 795 ALLNLSFNE-----EKDGSLEGETRKTQVQALDRFRAPFSF-----MLHALQSFCC 842
Db 799 ALLSSFSADSLAASDEDEM-----NNLQIAIGRIKLGIFAKAFLLGLLHG----- 846
QY 843 KRCRRKNSPKPKETESF-----AGENKDSILPDAR--PWKE---YDPMALYTGQA 889
Db 847 -----KILSPKDIWLSGEADGAGEAGETAPEDEKKEPPEDLKKNHILNHMGLA 900
QY 890 GAP-----LAPLAEVDDVEYCGGALPTSQHSAGVQAGDLPPET 930
Db 901 DGPPSSLEHLNFINNPLYLTIQVPIASESDLE-----MPTEE-----ET 941
QY 931 KQLTSPDDOGVEMEVFSEEDHLHSIQSPRKSDAYMSLSESTIDLNDIFRNLOKTV--S 988
Db 942 DTFSEPED-----SKPPQPLYDGNS--SVCSTADYKPPEDPEEQABEN 984
QY 989 PK-KQPRCFCPKGLSCHFLCHTKTKRSPWLVMMNIRKTCVOIKVHNSFESFIIFVILLS 1047
Db 985 PEGQPECECTEACVQRPCLYVDISQGRKKWTLRRACEKIVVHNWFEFIVFVILLS 1044
QY 1048 SGALIFEDVNLPSRQVEKLLRCTDNIFTFFLEMLKWKVAFGRFYTSANWCWLDPLI 1107
Db 1045 SGALAFEDIYTEQRVIRTILEYAKVFTYIFIMEMLLKWVAYGKVFYFTNACWLDPLI 1104

QY 1108 VVSVLSLM-----NLPSLKSFTLRALRPLRALSQFEGMKVYVYALISAIPLNVL 1160
Db 1105 VDSIISLVANWLGYSSELGPIKSLRTRALRPLRALSQFEGMRVYVYVALLGAIPSNVL 1164
QY 1161 LVCLIFLWLVFCILGVNLFSGKFGRCINGTDINMYLDETFEVPNRSOC-----NISNYSWKVP 1216
Db 1165 LVCLIFLWLVFSIMGVNLFAGFYICINTTSERF-DISEVNNKSECELSMHTGQVRLNV 1223
QY 1217 QVNDVNGVAYLALQVATYKGLWEIMNAVDSREKDPQDFEALYLYLVFVFWFIIFS 1276
Db 1224 KVNVDNVLGLYLSLLQVATEKGMWDIMYAAVDSREKEBPQYEVNLYMYLVFIIFS 1283
QY 1277 FFTNLFLVIGVINDFNQOQKLLGGODIFMTEQKYYNAMKGLTKKQKPTIPRLNKCQ 1336
Db 1284 FFTNLFLVIGVINDFNQOQKLLGGKDIEMTEQKYYNAMKGLSKKQKPTIPRPNKIQ 1343
QY 1337 AFVLDLTVSQVDFVTLILGLIVLNMIMMAESADQPKVKTFDIL--NIAFVVLFTTEC 1393
Db 1344 GMVYDLTVKQAFDITIMILICLNWTVMTVDQDS--QLKVDILLYNIMFIIFTGEC 1400
QY 1394 LIKVFALRQHYFTNGWNLFCVNVVLSIISTLSVLSLEDSDISFPPTLFRVVLARIGRL 1453
Db 1401 VLKMLALRQYFTVGNWIFDFVVTLSIVGLALSLLQK-YFVSPTLFRVIRLARIGRL 1459
QY 1454 RLVRAARGIRTLFALMMSLPSLNFNIGLLFLVMFYIIFGMSWFSKVKKSGIDDIENF 1513
Db 1460 RLIRGAKGIRTLFALMMSLPSLNFNIGLLFLVMFYIIFGMSWFSKVKKSGIDDIENF 1519
QY 1514 EFTFGSMCLCFQITTSAGWDITLLNPMLEA-----KEHCNSSQDSQOQPIAVVTFV 1565
Db 1520 EFTFGSIICLEFITTTSAGWDITLLNPMLEA-----KEHCNSSQDSQOQPIAVVTFV 1579
QY 1566 SYIIISFLIVVMYIAVILENPNATATESDPLGEDDEFEIFVWEKEDPEASQFIQYSA 1625
Db 1580 SYIIISFLIVVMYIAVILENPNATATESDPLGEDDEFEIFVWEKEDPEASQFIQYSA 1639
QY 1626 LSDFADALPEPLRVAKPNKQFLVMDLPMVMGDRHLCMDVLPFAFTTRVLGSSGLDWTMT 1685
Db 1640 LSDFVDTLQEPRLAKPNKIKLITLDPMPVPGDKTHCLDILFALTKEVLSGSGEMDLKQ 1699
QY 1686 MMEKFMANPEFKLYEPIVTTTRKEEEOGAAVIQRAYRKH 1728
Db 1700 TMEKFMANPEFKLYEPIVTTTRKEEEOGAAVIQRAYRKH 1742

RESULT 13

I51964

sodium channel alpha chain SCN4A, skeletal muscle - human

C:Species: Homo sapiens (man)

C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 20-Aug-1999

C:Accession: I51964

R:George, A.L.

Ann. Neurol. 31, 131-137, 1992

A:Title: Primary structure of the adult human skeletal muscle voltage-dependent sodi

A:Reference number: I51964; MUID:92246457

A:Accession: I51964

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1836 <RES>

A:Cross-references: GB:L04236; NID:g292485; PIDN:AA59624.1; PID:g292487

C:Genetics:

A:Gene: GDB:SCN4A

A:Cross-references: GDB:125181; OMIM:170500

A:Map position: 17q23.1-17q25.3

A:Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/

C:Superfamily: sodium channel protein

C:Keywords: duplication; skeletal muscle

Query Match 47.4%; Score 4347.5; DB 2; Length 1836;

Best Local Similarity 49.2%; Pred. No. 4.3e-315;

Matches 906; Conservative 272; Mismatches 416; Indels 249; Gaps 35;

QY 17 RPFTSDSLAAIKKRIATQKERR--KSKDKAAAEQPPRPQLDLKASRKLKPLKLYGIPPELV 74
D 18 RPFTRESLAALEQR-AVEEEARLQNKQMEIEEPERKPSRDLKAGNKLPMIYGPPPEVI 76
QY 75 TKPLEDLDPYKDKHTFWNLKKTITVRFSAKRALFILGPNPLRLSLMIRISVHSVSMF 134
D 77 GIPLEDLPYVSNKTTIVLNKKAIFRSATPALYLLSPESVVRGAIKVILHALFSMF 136
QY 135 IICVINCINCFMANSERSFNDIPEYVFIGIYILEAVIKILARGFIVDEFSLRDPNNW 194
D 137 IMITILNCVNTMSDPPPSKNV-EYFTGIYTFESLIKILARGFCVDDFTFLRDPNNW 195
QY 195 LDFIVIGTATATCPGSGQVNLALRFRFRALKAISVIGLKIVGALLRSVKKLVDVM 254
D 196 LDFSVIMAYLTERV-DLGNISALRTRFRVLRAKLTITVIGLKTIVGALIQSVKLSDMV 254
QY 255 VLTFLCLISFALVCOQLFMGLINQKCIKHNGCPNPAS- 292
D 255 ILTVCLSVFALVGLQLFMGNLRQKVR--WPPPFNDTNTWYSNDTWYGNEM 311
QY 293 -----KDCFEKE-----KDSBDFIMCGTWLGRPCPN 319
D 312 WYGNDSHWANDTNSHASWATNDTDFDWDAYISDEGNYFFLEGSNDALLCGNSDAGHCPCQ 371
QY 320 GSTCDKTTLPNDNNTKDFNGSWFLAMFRVMTQDSWERLYRQILRTSGIYFVFFVWVI 379
D 372 GYECIKTRPNYCYTSDYTFSWAFLALFLMTODYWENLFQTLRAAGKTYMIFVVI 431
QY 380 FLGSFYLLNLTLAVVWAYEQNRNVAATEAKEMFQEAQOOLREKEALVANGIDRSS 439
D 432 FLGSFYLLNLTLAVVWAYEQNRNVAATEAKEMFQEAQOOLREKEALVANGIDRSS 439
D 432 FLGSFYLLNLTLAVVWAYEQNRNVAATEAKEMFQEAQOOLREKEALVANGIDRSS 439
QY 440 LNSLQASSFSPPKRRKFGSKTRKSFMRGSKTAQA---SASDSDEDDASKNPQLLEQTKRL 496
D 483 -----EKAAQAALGEGEADGDPHAGKCNCGSLDTSQ 515
QY 497 SQNLVPDLFDEHVDPLHRQRALSVAISLITITIQEQKFOEPFCPCGNKLSKYLWDCSP 556
D 516 EKGAP-----RQSGSGSDGISDAMEELEAHQKPPWYKCAHKVLIWCCA 562
QY 557 QWLCIKKVLRTIMTDPTELAITTCIINTVFLAVEHHNMDNLTILKIGNWFTGIFI 616
D 563 PWLFKNIHILVNDPFDVLTGICVILNTLFMAHEYPMTFHDNVLTVGNLVTGIFT 622
QY 617 AEMCLKIATLDPHYFRHGNVDSIVALLSLADY-LYNTLSDNRSFLASLRLVRPKL 675
D 623 AEWVLLIAMPYEFYQOGWNIFDSIIVTSLVELGLANV---OGLSVLRSLRLVRPKL 679
QY 676 AKSWPTLNTLTKIICHVSGALGNLTIVVITVIFSVGMRLFGTKFNK-TAYATQERPR 734
D 680 AKSWPTLNTLTKIICHVSGALGNLTIVVITVIFSVGMRLFGTKFNK-TAYATQERPR 734
QY 735 RRVHMDNFYSLVVFVRLCGEWENTENMWGMQMDGSPCLTIIVFLVIMVIGKLVVNLFI 794
D 740 PRWHMDNFYSLVVFVRLCGEWENTENMWGMQMDGSPCLTIIVFLVIMVIGKLVVNLFI 794
QY 795 ALLNLSFSNE-----EKDGSLEGETRKTQVOLALDRPRRAFSE-----MLHALQSPCC 842
D 799 ALLNLSFSNE-----EKDGSLEGETRKTQVOLALDRPRRAFSE-----MLHALQSPCC 842
QY 843 KKCRRRKSPKPKETTESF-----AGENKDSILDPAR--PWKE--YDFDMALYTGQA 889
D 847 -----KILSPKIMLSIGEADGAGEGETAPEDEKKEPPEDLKKNHILNHHGLA 900
QY 890 GAP-----LAPLAEVDDVEYCGEGALPTSQHSAGVQAGDLPPEP 930
D 901 DGPPSSLELDHLNFINNPYLTIQVPIASESDLE-----MPTEE-----ET 941
QY 931 KULTSPDQGVMEVFSEEDLHLISQSPKSDAVSMLSECTIDLNDIFRNLOKTV--S 988
D 942 DTFSEPED-----SKPPQPLYDGN--SVCSTADYKPPPEEDPEQABEN 984

QY 989 PK-KOPDRCPFKGLSCHFLCHKTDKRKSPWVLMNIRKTCYOIVKHWSFESFIIFVILLS 1047
D 985 PEGEQPEBCTEACVORMPCLYVDITSQGRKKKWTTLRRACKFIVHNHNFETIFVEMILLS 1044
QY 1048 SGALIFEDVNLPSRPOVEKLLRCDTNIPTFIFLLEMLKWAFAFGRRFTTSANWCLDFLI 1107
D 1045 SGALAFEDIYTEQRRVIRITILEYADKVFTYIFIMEMLLKWAFAFGRRFTTSANWCLDFLI 1104
QY 1108 VVWSVLSUM-----NLPSLKSEFTLRALPLRALSQFEGMKVWVVALISAIPAILANVL 1160
D 1105 VDVSIISLVANWGLYSELGPIKSLRTLRALPLRALSQFEGMKVWVVALISAIPAILANVL 1164
QY 1161 LVCLIFWLVFCILGVNLFSGKRCINGCTDINMYLDFTEVPPNRSC-----NISNYSWKVP 1216
D 1165 LVCLIFWLVFCILGVNLFSGKRCINGCTDINMYLDFTEVPPNRSC-----NISNYSWKVP 1216
QY 1217 QVNFEDVGNAYLALLQVATYKGLWEIMNAADVDSREKQPOFEANLYAYLVFVPIIFGS 1276
D 1224 KVNVDNVLGYSLLQVATYKGLWEIMNAADVDSREKQPOFEANLYAYLVFVPIIFGS 1283
QY 1277 FFTNLNLTGVIIDNPNQOKKLGQDIFEMTEEQKYYNAMKGLTKPKQKPIPRPLNCKQ 1336
D 1284 FFTNLNLTGVIIDNPNQOKKLGQDIFEMTEEQKYYNAMKGLTKPKQKPIPRPLNCKQ 1336
QY 1337 AFVEDLVTQSFVDVIIIGLIVNLMIIMAESADQPKDKTKFTDIL---NIAFVWIFTTEC 1393
D 1344 GMVYDLVTQAFDITIMILICLNVMVMTDDQS---QLKVDILYNINMIFIIFTGEC 1400
QY 1394 LIKVPALROHFTNGWNLFDVWVVSIIISLVSRLSDSDISFPPTLFRVVLARIGRIL 1453
D 1401 VLKMLARQYFTVGNWIFDFVWVVSIIISLVSRLSDSDISFPPTLFRVVLARIGRIL 1459
QY 1454 RLVRAARGIRTLFALMWSLPSLNFIGNLGLLFLVWFIYAFGMWSFKVYKGGIDDIENF 1513
D 1460 RLKIRAKGIRTLFALMWSLPSLNFIGNLGLLFLVWFIYAFGMWSFKVYKGGIDDIENF 1519
QY 1514 EFTGSMCLFQITTSAGWDTLLANPMEA-----KEHCNSSQSDSQOQIAVVFV 1565
D 1520 EFTGSMCLFQITTSAGWDTLLANPMEA-----KEHCNSSQSDSQOQIAVVFV 1565
QY 1566 SYIIISFLIVNMYIAVLENFNTATESEDPGLGEDDEIFEYVWEKFDPEASQIQISA 1625
D 1580 SYIIISFLIVNMYIAVLENFNTATESEDPGLGEDDEIFEYVWEKFDPEASQIQISA 1639
QY 1626 LSDFADALPELRLVAKPNKQFLVMDLPMVGMRLHCHMDVLFATVTVLGGSSGDLTKKT 1685
D 1640 LSDFADALPELRLVAKPNKQFLVMDLPMVGMRLHCHMDVLFATVTVLGGSSGDLTKKT 1685
QY 1686 MNEKFMENANPKLYEPIVTTTKRKEEEOGAAVIAQRAYRKH 1728
D 1700 TMEKFMENANPKLYEPIVTTTKRKEEEOGAAVIAQRAYRKH 1728
RESULT 14
JS0648
Sodium channel alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: JS0648; A42099
R:Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A:Title: Sequence and genomic structure of the human adult skeletal muscle sodium ch
A:Reference number: JS0648; MUID:92134303
Z:Accession: JS0648
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
R:Residues: 1-1836 <WAS>
A:Note: 861-Asp was also found as the result of polymorphism
R:McClatchey, A.I.; Van den Bergh, P.; Pericak-Vance, M.A.; Raskind, W.; Verellen, C.
Cell 68, 769-774, 1992
A:Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of th
A:Reference number: A42099; MUID:92154689
Z:Accession: A42099

A: Molecule type: DNA
A: Residues: 1299-1351 <MC>
A: Cross-references: GB:S82622; NID:g245611; PIDN:AAB21450.1; PID:g245612
A: Experimental source: skeletal muscle
A: Note: sequence extracted from NCBI backbone (NCBIN:82622, NCBI:P:82623)
C: Genetics:
A: Gene: GDB:SCN4A
A: Cross-references: GDB:l125181; OMIM:170500
A: Map position: 17q23.1-17q25.3
C: Superfamily: sodium channel protein
C: Keywords: duplication; glycoprotein; phosphoprotein; transmembrane protein
F: 129-150/Domain: transmembrane #status predicted <TR1>
F: 159-178/Domain: transmembrane #status predicted <TR2>
F: 191-210/Domain: transmembrane #status predicted <TR3>
F: 217-236/Domain: transmembrane #status predicted <TR4>
F: 253-266/Domain: transmembrane #status predicted <TR5>
F: 424-449/Domain: transmembrane #status predicted <TR6>
F: 574-597/Domain: transmembrane #status predicted <RI1>
F: 609-632/Domain: transmembrane #status predicted <RI2>
F: 641-660/Domain: transmembrane #status predicted <RI3>
F: 667-686/Domain: transmembrane #status predicted <RI4>
F: 702-724/Domain: transmembrane #status predicted <RI5>
F: 777-802/Domain: transmembrane #status predicted <RI6>
F: 1027-1049/Domain: transmembrane #status predicted <II1>
F: 1064-1089/Domain: transmembrane #status predicted <II2>
F: 1096-1116/Domain: transmembrane #status predicted <II3>
F: 1122-1143/Domain: transmembrane #status predicted <II4>
F: 1163-1184/Domain: transmembrane #status predicted <II5>
F: 1269-1295/Domain: transmembrane #status predicted <II6>
F: 1349-1372/Domain: transmembrane #status predicted <VI1>
F: 1384-1407/Domain: transmembrane #status predicted <VS2>
F: 1414-1437/Domain: transmembrane #status predicted <VS3>
F: 1447-1469/Domain: transmembrane #status predicted <VS4>
F: 1485-1507/Domain: transmembrane #status predicted <VS5>
F: 1574-1598/Domain: transmembrane #status predicted <VS6>
F: 21, 149, 220, 378, 415, 1019, 1130, 1242, 1313, 1721, 1826/Binding site: phosphate (Thr) (covalent)
F: 56, 251, 513, 653, 1511, 1746/Binding site: phosphate (Ser) (covalent) (by protein kinase A)
F: 214, 288, 291, 297, 303, 315, 321, 333, 362, 507, 702, 961, 1191, 1205/Binding site: phosphate (Ser) (covalent) (by protein kinase A)
F: 246, 670, 725, 850, 950, 1127, 1195, 1328/Binding site: phosphate (Thr) (covalent) (by protein kinase A)
F: 387, 457/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

Query Match	47.3%	Score 4342;	DB 2;	Length 1836;
Best Local Similarity	49.0%;	Pred. No. 1.1e-314;		
Matches	908;	Conservative 274;	Mismatches 422;	Indels 250;
Gaps	36;			
Qy	7	PVIPP-DERNFRPPTDSLAIAIKRIAIQKERK--KSKDKAAAEPPQRPOLDLKASRKL	63	
Db		: : : : : : : : :		
Qy	7	PMVLPLGECRLPPTRESLAAIEOR-AVEEARLQRKWKQMEIEPERKPRSDUEAGNLP	65	
Db		: : : : : : : : :		
Qy	64	KLYGDIPPELVTRPLEDDPYKYDKDHTFMVLNKKRTIYFSAKRALFILGPFNPLRSLMI	123	
Db		: : : : : : : : :		
Qy	66	MIYGDPPPEVIGPLEDDPYVTNNKKTIVILMKGKAIFRSATPALYLLSPFSVVRGAI	125	
Db		: : : : : : : : :		
Qy	124	RISVHSVFSFIICTVIINCMFMANSMERSFDDNDIPEYFVIGIYILEAVIKILARGFIVD	183	
Db		: : : : : : : : :		
Qy	126	KVLIIHALFSFIMITILTNCFVTMSPDPPMWSKNV-EYTFGIYTFESLIKILARGFCD	184	
Db		: : : : : : : : :		
Qy	184	EFSELRDPNNWLDPIVIGTATATCFPGSQVNLSALRFRFRVRALKAIASVIGLKVIYGAL	243	
Db		: : : : : : : : :		
Qy	185	DTFLRDPNNWLDPSVIMMAYLTFEV-DLGNISALRFRVLRALKTTIVTIGLKTIVGAL	243	
Db		: : : : : : : : :		
Qy	244	LRSVKKLVDMVWLTFCLSTFALVQGLFNGILNQKCIKINCGPNASN-----	292	
Db		: : : : : : : : :		
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Db		: : : : : : : : :		
Qy	293	-----KDCFEK-----KDESEFIMC	308	
Db		: : : : : : : : :		
Qy	301	YGNDTWYGNEMWYGNDSWYANDTWSHAWATNDTFDWDAYISDEGNFYFLEGSNDALLC	360	
Db		: : : : : : : : :		
Qy	309	GTWLGSRPCNGSTCDKTTILNPNNNTYKTFNGFWSFLAMFRVMTQDSWERLYQILRTSG	368	
Db		: : : : : : : : :		
Qy	361	GNSSDAGCHGEGECIKTGRNPNYGYTSYDTSFWAFVLFALFRLMTQDYWNELFOLTTAAAG	420	
Db		: : : : : : : : :		

Db 1284 FFFLNLFVGIIDNFNOQKK--GKDIFFMTEEQKYYNAMKLGSKKPKQKIPRPQNKIQ 1342
Qy 1337 AFVDELVTQVEDVILIGLIVLNIMMAESADOPKDVKTFDIL---NIAFVVIETJEC 1393
Db 1343 GMYDLVTQKAFDTIMILICLNVMVTMVTDNQS---QLKVDILYNINMIFIIIFTGEC 1399
Qy 1394 LIKVPALRQHFTNGWNLFDCVVVLSIISTLVSRLESDISFPPTLFRVVRLARIGRIL 1453
Db 1400 VLKMLALRQYVFTVGWNIFDVFVILSIVGLALSDLIQK-YFVSPTLFRVIRLARIGRVL 1458
Qy 1454 RLVRARIGIRTLFALMMSLPSLENIGLLFLVFIYAFGMSWFSKVYKSGIDDIINF 1513
Db 1459 RLIRGAKGIRTLFALMMSLPALENIGLLFLVFMFIYSIFGMSNFAYVYKESGIDDMENF 1518
Qy 1514 ETFTGSMCLCFQITTSAGWDTLNPMLEA-----KEHCNSSQSDSCQOPOIAYVYFV 1565
Db 1519 ETFGNSIICLFEITTSAGWDGLLNPLNSGPPDCDPLNLEPGTSVKGDCGNPSIGICFFC 1578
Qy 1566 SYIIISFLIVVMYIAVILENFNTATESEDPLEDDEFEIYEVWEKFDPEASOFIOYSA 1625
Db 1579 SYIIISFLIVVMYIAIILENFVATESESEPLEDEDEFEYETWEKEDPDATQFIAYSR 1638
Qy 1626 LSDFADALPEPLRVAKPNKFVNDLPMVMGDRLHCMVDLFAFTTRVLGSDSSGLDTMKT 1685
Db 1639 LSDFVDTLQEPRLIAKPNKIKLITLDLPMVPGDKIHCILDLTALTKEVLGSDGEMDALQ 1698
Qy 1686 MMEKEFEANPFKKLYEPVITTTTKRKEEQGAAVIQRAYRKH 1728
Db 1699 TMEKEFMAANPSKVSYPEITTTTLKRKHEEVCIAIKIQRAYRHL 1741

Search completed: February 27, 2002, 01:30:22
Job time: 9627 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2002, 01:29:01 : Search time 67.45 Seconds
(without alignments)
959.428 Million cell updates/sec

Title: US-09-646-224A-2

Perfect score: 9173

Sequence: 1 MEERYYPVFPDERNRPPT.....VFCNGDLSLDVAKVKVHND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4724	51.5	2019	1	CIN5_RAT
2	4711.5	51.4	2016	1	CIN5_HUMAN
3	4502	49.1	2005	1	CIN2_HUMAN
4	4496.5	49.0	1951	1	CIN3_RAT
5	4496	49.0	2009	1	CIN1_HUMAN
6	4493.5	49.0	1951	1	CIN3_HUMAN
7	4484.5	48.9	2005	1	CIN2_RAT
8	4476	48.8	2009	1	CIN1_RAT
9	4363.5	47.6	1840	1	CIN4_RAT
10	4347.5	47.4	1836	1	CIN4_HUMAN
11	3983	43.4	1820	1	CIN4_ELEL
12	3524.5	38.4	2131	1	CIN4_DROME
13	3184	34.7	1682	1	CIN6_HUMAN
14	2945	32.1	1522	1	CIN1_LOLBL
15	1508.5	16.4	1687	1	CCAM_MUSDO
16	1497.5	16.3	1873	1	CCAS_RABIT
17	1496	16.3	1873	1	CCAS_HUMAN
18	1482	16.2	2190	1	CCAD_CHICK
19	1481	16.1	2203	1	CCAD_RAT
20	1478	16.1	1835	1	CCAI_RAT
21	1475.5	16.1	1610	1	CCAD_MESAU
22	1473	16.1	2139	1	CCAC_MOUSE
23	1472	16.0	2161	1	CCAD_HUMAN
24	1469	16.0	2221	1	CCAC_HUMAN
25	1460	15.9	1852	1	CCAS_CYPFA
26	1456	15.9	2171	1	CCAC_RABIT
27	1453	15.8	2212	1	CCAA_RAT
28	1452	15.8	2326	1	CCAB_DISOM
29	1448.5	15.8	2169	1	CCAC_RAT
30	1443	15.7	2516	1	CCAD_HUMAN
31	1439.5	15.7	1966	1	CCAF_HUMAN
32	1438	15.7	2272	1	CCAE_MOUSE
33	1437.5	15.7	2223	1	CCAE_DISOM

34	1437	15.7	2164	1	CCAA_MOUSE
35	1434.5	15.6	2222	1	CCAE_RAT
36	1431	15.6	2353	1	CAAH_HUMAN
37	1430.5	15.6	2312	1	CCAE_HUMAN
38	1426.5	15.6	2339	1	CCAB_RABIT
39	1422.5	15.5	2254	1	CCAG_RAT
40	1421	15.5	2259	1	CCAE_RABIT
41	1412	15.4	2339	1	CCAB_HUMAN
42	1407	15.3	2336	1	CCAB_RAT
43	1405	15.3	2424	1	CCAA_RABIT
44	1404.5	15.3	2505	1	CCAA_HUMAN
45	1402	15.3	2377	1	CCAG_HUMAN

ALIGNMENTS

RESULT 1

FD	CIN5_RAT	STANDARD;	PRT;	2019 AA.
AC	P15389;			
DT	01-APR-1990 (Rel. 14, Created)			
ET	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE ALPHA-SUBUNIT.			
GN	SCN5A.			
QS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RX	MEDLINE=90046760; PubMed=2554302;			
RA	Rogart R.B., Cribbs L.L., Muglia L.K., Kephart D.D., Kaiser M.W.;			
RT	"Molecular cloning of a putative tetrodotoxin-resistant rat heart Na+			
RL	channel isoform."			
CC	Proc. Natl. Acad. Sci. U.S.A. 86:8170-8174(1989).			
CC	PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE-DEPENDENT SODIUM ION			
CC	MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT. IT IS A TETRODOTOXIN-RESISTANT NA+ CHANNEL ISOFORM.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5			
CC	HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED			
CC	SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	-1- MISCELLANEOUS: NA+ CHANNELS IN MAMMALIAN CARDIAC MEMBRANE HAVE			
CC	FUNCTIONAL PROPERTIES QUITE DISTINCT FROM NA+ CHANNELS IN NERVE			
CC	AND SKELETAL MUSCLE.			
CC	-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.			

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EMBL; M27902; AAA42114.1; -;
PIR; A33996; A33996;
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR000048; IQ.
InterPro; IPR001696; Na_channel.
Pfam; PF00520; ion_trans; 4.
Pfam; PF00612; IQ; 1.
PRINTS; PR00170; NACHANNEL.

Db 898 VGMQLFGSKYKCEVCISKNDCELP--RWHMDFHPSFLVFRVLGGEWETMWDGM-EVA 954
Qy 770 GSPCLIVFVLMVIGKVLNLFALLNLSFNEKDGSLGETRKTGVOLALDRFRRA 829
Db 955 GQTHCLTVFMVWVIGNVLVNLFLALLLSSESSNL--AATDDNEMNQLIAGRMQKG 1013
Qy 830 FSEMLHALQSCCKCRKRKNSP---KPKETTESFAGNKDSILDPARPKKEYDMDALY 885
Db 1014 IDFKVRKIRFQAFVRKQKALDEIKPLEDLNN---KDCISN----- 1055
Qy 886 TQAGAPLAPLAEDVDEYCEG-----GALPTSHSAGVQAGD---LPPETKOLTS- 936
Db 1056 -----HTTETGKDLNLYKDGNGTTSIGSSVYKVVDESDYMSFINPSLTVTVPI 1107
Qy 937 -----DDOGVEMEVFSEEDLHLSIQSPRKSDAVSMLSECSFTIDLNFRLNKTQVSPKK 991
Db 1108 AVGESDFENLTERFSSS---DWEESKEKLNATSS--SEGSTVDIGAPAEQEPVEPEE 1163
Qy 992 --QDRCFPKGLSCHFLCHKTKDKRSPWVLMNIRKTCYQVKKHSWFESFIIFVILLSSG 1049
Db 1164 SLEPEACFTDCVRKFKCCQISIEBGKGLWNLRLKTCYKIVHNWETFTIVEMILLSSG 1223
Qy 1050 ALIFEDVNLPSRQVEKILRLCTDNFTIFILEMLKVAFGFRYFTSANCWLDFLIV 1109
Db 1224 ALAFEDIYEQRTIKTMLEYADKVTYFIFILEMLKVAFGFRYFTSANCWLDFLIV 1283
Qy 1110 VSLVSL-----MNLPSLKFRTLRALRALSOFQGMKVYVYALISAIPAILNVLV 1162
Db 1284 VSLVSLTANALYSELGAIKSURLRALRPLRALSFRGMRVAVNALLGALIPSIMNVLV 1343
Qy 1163 CLIFLWFCILGNVLSFGKFGRCINGTDINMYLDFTEPNRSQCNI---SNYS--WKYPQ 1217
Db 1344 CLIFLWFCILGNVLSFGKFGRCINGTDINMYLDFTEPNRSQCNI---SNYS--WKYPQ 1402
Qy 1218 VNFDMVNGYALALQVARYKGLWLEIMNAVDSREKDEQDPDEANLYAVLYFVFIIFGSF 1277
Db 1403 VNFDMVNGYALALQVARYKGLWLEIMNAVDSREKDEQDPDEANLYAVLYFVFIIFGSF 1462
Qy 1278 FTNLNFIQVIGIDNFNOQKGLGGQDIFMTEQKYYNNAKMLGTGKPKPPIRPLNKKQA 1337
Db 1463 FTNLNFIQVIGIDNFNOQKGLGGQDIFMTEQKYYNNAKMLGTGKPKPPIRPLNKKQA 1522
Qy 1338 FVFDLVTSQVDFVILGLVILNMIMMAESADQPKDKKTKFDILNIAFVFIIFGLIKV 1397
Db 1523 MVFDFVTKQVEDISTMILICLNMVMTVETDDQSQEMNLYWILVFLVFTGECVLK 1582
Qy 1398 FALROHYFTGNWLNFDVGVVLSIISLTVSRL--EDSDISFPPTLFRVRLARIGRILRV 1456
Db 1583 ISLRYFTYFTGNWLNFDVGVVLSIISLTVSRL--EDSDISFPPTLFRVRLARIGRILRV 1640
Qy 1457 RAARGIRTLFALMMSLPSLNFIGNLGLLFLVMFVIYAFIAGMSWFSKVKKGSGIDDFNFETF 1516
Db 1641 KGAKGIRTLFALMMSLPSLNFIGNLGLLFLVMFVIYAFIAGMSWFSKVKKGSGIDDFNFETF 1700
Qy 1517 TGSMLCLFQITTSAGWDTLNPMLEA-----KEHCNSSQSDSCQOPQIATVYFVSII 1568
Db 1701 GNSMCLFQITTSAGWDTLNPMLEA-----KEHCNSSQSDSCQOPQIATVYFVSII 1760
Qy 1569 IISFLVNMVYIAVILENFATETESDEPLGDEFEIYEWKEDPEASQFIQYISALSD 1628
Db 1761 IISFLVNMVYIAVILENFATETESDEPLGDEFEIYEWKEDPEASQFIQYISALSD 1820
Qy 1629 FADALPELRLVAKPKKQFVLMVMDLPMVMDRLHCLMDVLFATFTRVLGDSGLDWTWKWME 1688
Db 1821 FADALPELRLVAKPKKQFVLMVMDLPMVMDRLHCLMDVLFATFTRVLGDSGLDWTWKWME 1880
Qy 1689 EKFMANPKFKLYEPIVTTTRKEEQAQAAVIOQARYKHM-----EKMKVRLKDRSSS 1743
Db 1881 ERFMASNP SKVSYEPITTTTLRKQEVSAIIIQARYRYLLKQKVKVSYIKDKGRE- 1939
Qy 1744 HQVFCNG 1750
I: I

1940 ----CDG 1942
Db 1940 ----CDG 1942
RESULT 4
CIN3_RAT STANDARD; PRT: 1951 AA.
XO CIN3_RAT
AC P08104;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SODIUM CHANNEL PROTEIN, BRAIN III ALPHA SUBUNIT (VOLTAGE-GATED SODIUM CHANNEL SUBTYPE III).
DE CHANNEL SUBTYPE III).
GN SCN3A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=88137594; PubMed=2449363;
KA Kavano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
KT "Primary structure of rat brain sodium channel III deduced from the cDNA sequence.";
RL FEBS Lett. 228:187-194(1988).
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -!- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
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CC EMBL; Y00766; CAA68735.1; -
DR PIR; S00320; S00320.
DR InterPro; IPR002111; Cat_channel_Trpl.
DR InterPro; IPR000636; Catlon_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR Pfam; PF00520; Ion_trans. 4.
DR Pfam; PF00612; IQ_1.
DR PRINTS; P000170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
KW Ionic channel; transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Multigene family.
FT TRANSMEM 124 147 S1 OF REPEAT I.
FT TRANSMEM 156 175 S2 OF REPEAT I.
FT TRANSMEM 189 207 S3 OF REPEAT I.
FT TRANSMEM 214 233 S4 OF REPEAT I.
FT TRANSMEM 249 273 S5 OF REPEAT I.
FT TRANSMEM 401 426 S6 OF REPEAT I.
FT TRANSMEM 706 730 S1 OF REPEAT II.
FT TRANSMEM 742 765 S2 OF REPEAT II.
FT TRANSMEM 774 793 S3 OF REPEAT II.
FT TRANSMEM 800 820 S4 OF REPEAT II.

FT TRANSMEM 836 856 S5 OF REPEAT II. S5 OF REPEAT II. 519
FT TRANSMEM 910 935 S6 OF REPEAT II. S6 OF REPEAT II. 519
FT TRANSMEM 1153 1176 S1 OF REPEAT III. S1 OF REPEAT III. 519
FT TRANSMEM 1190 1215 S2 OF REPEAT III. S2 OF REPEAT III. 519
FT TRANSMEM 1222 1243 S3 OF REPEAT III. S3 OF REPEAT III. 519
FT TRANSMEM 1248 1269 S4 OF REPEAT III. S4 OF REPEAT III. 519
FT TRANSMEM 1289 1310 S5 OF REPEAT III. S5 OF REPEAT III. 519
FT TRANSMEM 1333 1419 S6 OF REPEAT III. S6 OF REPEAT III. 519
FT TRANSMEM 1473 1496 S1 OF REPEAT IV. S1 OF REPEAT IV. 519
FT TRANSMEM 1508 1531 S2 OF REPEAT IV. S2 OF REPEAT IV. 519
FT TRANSMEM 1538 1561 S3 OF REPEAT IV. S3 OF REPEAT IV. 519
FT TRANSMEM 1572 1593 S4 OF REPEAT IV. S4 OF REPEAT IV. 519
FT TRANSMEM 1609 1631 S5 OF REPEAT IV. S5 OF REPEAT IV. 519
FT TRANSMEM 1698 1722 S6 OF REPEAT IV. S6 OF REPEAT IV. 519
FT CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 835 835 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 1002 1002 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 1019 1019 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
FT CARBOHYD 1331 1331 N-LINKED (GLCNAC. .) (POTENTIAL). (POTENTIAL). 519
SQ SEQUENCE 1951 AA: 221385 MW: 745E851524BD10E CRC64; 519

Query Match 49.0%; Score 4496.5; DB 1; Length 1951;
Best Local Similarity 49.0%; Pred. No. 3e-277;
Matches 945; Conservative 282; Mismatches 444; Indels 257; Gaps 36;

QY 11 PDERNFRPFTSDSLAAIKRIATQKERRKDKD-AAAPQPPQRLDLDKASRLKPLKLYGDI 69
DB 9 PCPESFLRFTRESLAAIEKRAAEKAKPKKEQDIDDKPKPNSDLEAGKPLPIYGD 68
QY 70 PPELVTKPLEDDPYVYKHKTFTWLNKRTTYRFSAKRALFTLGFNPNPLRSLMTRISVHS 129
DB 69 PPEVSEPLEDDPYVYVSKKFTVVLNKGKATFRFSATSALYILTLPLNPKVIAIKILVHS 128
QY 130 VFSMFIICITVINCMANSMERSFDNDIPEVVFVGIIVLEAVIKILARGFTVDFEFLR 189
DB 129 LFSMLMCIILNCFVMTLSNPPDKNV-EYTFGFIYFESLILKILARGCFDFTFLR 187
QY 190 DPWNMLDFVIGTATATCPGSOVNLALRTRFRFRALKALISVISGLKVIIVGALLRSYKK 249
DB 188 DPWNMLDFSVIMAYVTEFV-DLGNVSALRTRFRVLRLAKLTISVIPGLKTIVGALLQSYKK 246
QY 250 LVDVWVLTLFCLSLFALYGOQLFMGILNOKIKIKHCGNPNASNKDCPKEKDS----- 302
DB 247 LSDVMILTAVCLSVFALIGLQFMGNLRNKGQW-----PPSD-SAFETNTTSYFNGTMD 300
QY 303 -----EDFTMCGTWLGSRCPCNGSTCDKTLNPD 331
DB 301 SNGTFVNTMTFNKWDYIADDSHYVLDGQKDPDLCNGSDAGOCPEGYICVKGARPN 360
QY 332 NNYTKDFNGSFLAMFVMTQDSWERYLYQLRTSGTYFFVFFVVFVIFLGSFYLLNLTL 391
DB 361 YGYTSDFDTSNAFLSLFRMTQDYENLYQLTLRAAGKTYMTFFVLVIFLGSFYLVNLIL 420
QY 392 AVVTMAYEQNRNVAETEAKMPQEAQQLLREPEKALVAM-----GIDR 437
DB 421 AVVAMAYEQNAATLEEAQEAQEQMQLKQOEAQAAVAAASAAASDFSGIGGLGE 480
QY 438 SSLSLQASFSPPKKEFGS---KTRKSEFMRSKTAQAS---ASDSEDDASK----- 485
DB 481 LLESSEASKLSSKSAKEWRNRKRQRHLEHGRHNRADGRFPKSESEDSVKRRSFLLS 540
QY 486 ---NPQLEQTKRL-----SONLPVDLF-----DEH 508
DB 541 LDGNP--LJTGDKLCSPHQSLLSIRGSLFSPRNSKTSIFPRGRKADGVGSENDPADDEH 598

509 -----VDPHQRALS 519
599 STFDESESRDLSLVPHRPGERRNSNGTTTETEVKRRLLSYQISMWLEDDSSGQRMS 658
520 AVSILITITIQOEKFOEPCPCGNLASKYLWDCSPWLCKIKVLRITMDTPPELAI 579
659 IASILTNTWEELESROKPCPCWYRANVFLWDCDCLWKLVLNVLVMDPFVDLAI 718
580 ICIINTVFLAVEHHNMDNLKILKIGNVFTGIFIAEMCLKIIALDPIHYFRHWNV 639
719 ICIVLNTLFMAHEHYPMTOQSSVLTGNLVTGIFTAEVVLKIIAMDPIYVQEGWIF 778
640 DSIYALLSLADV-LYNTLSNDRSPLASLRLVRPKLAKSWPTLNLKILKIGHSVGALGN 698
779 DGIIVLSLMEIGLANV---EGLSVLRSFRLLRVFKLAKSWPTLNLKILKIGHSVGALGN 835
699 LTVLTVIVVFVSVVGMRLFGTKENK-TAYATQERPRRRWMDNFYHSLFVVRILCGEW 757
836 LTLVLAIVFVAVVGMQLFGKSKYCKINVDCKLPRWMDNFHSLFVVRILCGEW 895
758 TENMGCMQDDGSPCLIIIVFLIMVIGLVNLNFIALLNSFNEEKDGSEGETRKT 817
896 IETMWDCA-EVAGQTMCLIVEMLVNIGLVNLNFIALLNSFSSDNL-AATDDDNEMN 953
818 KVQALDRPRRAFSPMLHALQSFCCKKCRK---NSRPKKTETTESFAGENKDSILLDARP 874
954 NLOIYVGRMKGIDFVKNKI-----RECRAFRKPKVIEIQEG----- 993
875 WKEYDMDALYTGQAGAPLAPEVEDDVEYCGEGALPTSOHSAGVAGO----- 925
994 -NKIDSCMSNNTG-----IEISKELNYLKDNGT-----TSGVTGSSVEKYVIDE 1038
926 -----LPEETKQLTSP-----DDQGVEMEVSSEDLHLSTQSPKSKSDAVSMISEGT 973
1039 NDYMSFINNPSLTVTVPVAVGESDENLNTBEFSSES---ELEESKEKLNATSS-SEGT 1094
974 IDLNDIFNLKOTVSPKK--QPDRCFPKGLSCHFLCHTKDRKSPWLWNLNIRKTCYQIV 1031
1095 VDVAPPREGEOAEIEPEDLKAPEACFEGCCKKFPFCQVSTBEGKGIWNLNIRKTCYSTV 1154
1032 KHSNPESFIIFVILLSSGALIFEDVNLSPQVEKLLACTONITFIILLEMILKAWFG 1091
1155 EHNPFETIFVILLSSGALAFEDIYEQRTIKTMEYADKVFTIILEMLLKAWYAG 1214
1092 FRRYTSAMCWLDLIVVSVLSL-----NLPKLSFRTRLRALRPLRALSOPFGMK 1144
1215 FQYFTNAMCWLDLIVDLSVLSVANALGYSELGAIKSLRTRLRALRALSREFGMV 1274
1145 VYALISAIPAILNVLVCLIFVLCILGNVLSGKFGRCINGTDINMLDFTVEPNRS 1204
1275 VVNALVGAIPSIMNVLLVCLIFVLFISIMGNVLFAGKYHCVTNTTGNMF-EIKEVNNFS 1333
1205 QCN1--SNYSKMPQOVNFDNVGNVALLOVATYKGLWLEIMNAADVDSREKDEQDFEALN 1262
1334 DQALGKQARKNVKNVFNNDNVGAGYLLQVATFGWMDIMYAAVDSRDXLQPIYEENL 1393
1263 YAYLVVYFIIIFGSPFTLNLFIIDNFNOOKKLGQDIFMTEEQKKYNNAMKLGTK 1322
1394 YMYLVYFIIIFGSPFTLNLFIIDNFNOOKKFGQDIFMTEEQKKYNNAMKLGSK 1453
1323 KPQRPRLPNKQAFVFDVLTQVDFVILIGLIVLNMIIMAESADQPKVKYKTFDILN 1382
1454 KPQRPRLPNKQAFVFDVLTQVDFVILIGLIVLNMIIMAESADQPKVKYKTFDILN 1513
1393 IAFVVFIECLIKVFAHQHYFTNGWNLFDQVNVVLSITISPLVSL-EDSDISFPPTLF 1441
1514 LVFVILFTEFLKULISURYIFTIGWNIFDFVNVVILSVGMFLAELEKTFVS--PTLF 1571
1442 RVVRLARIGRLVRAARGITLFLALMMSLPSLNFILGLLFLVYMFYIYAFGMSWFSKV 1501
1572 RVIRLARIGRLRLKAGKIGITLFLALMMSLPSLNFILGLLFLVYMFYIYAFGMSWFSKV 1631

- I- DISEASE: DEFECTS IN SCN1A ARE THE CAUSE OF GENERALIZED EPILEPSY WITH FEBRILE SEIZURE PLUS TYPE 2 (GEFS-2). THIS AUTOSOMAL DOMINANT DISORDER IS CHARACTERIZED BY FEBRILE SEIZURES IN CHILDREN AND AFBRIE SEIZURES IN ADULTS. PENETRANCE IS INCOMPLETE AND A LARGE INTRAFAMILIAL VARIABILITY OF THE PHENOTYPE IS OBSERVED.

- I- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

- I- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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EMBL; S71446; AAB31605.1; --
EMBL; X65362; CAA46439.1; --
EMBL; M91803; -- NOT_ANNOTATED_CDS.
PIR; S29184; S29184.
MIM; 182389; --
MIM; 604233; --
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR000048; IQ.
InterPro; IPR001696; Na_channel.
Pfam; PF00520; Ion_trans; 4.
Pfam; PF0612; IQ; 2.
SMART; SM00015; IQ; 1.

IONIC channel; transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Multigene family; Disease mutation.

REPEAT 110 454
I (BY SIMILARITY).
REPEAT 750 1022
II (BY SIMILARITY).
REPEAT 1200 1514
III (BY SIMILARITY).
REPEAT 1523 1821
IV (BY SIMILARITY).
TRANSMEM 124 147
S1 OF REPEAT I (BY SIMILARITY).
TRANSMEM 156 175
S2 OF REPEAT I (BY SIMILARITY).
TRANSMEM 189 207
S3 OF REPEAT I (BY SIMILARITY).
TRANSMEM 214 233
S4 OF REPEAT I (BY SIMILARITY).
TRANSMEM 250 273
S5 OF REPEAT I (BY SIMILARITY).
TRANSMEM 400 425
S6 OF REPEAT I (BY SIMILARITY).
TRANSMEM 763 827
S1 OF REPEAT II (BY SIMILARITY).
TRANSMEM 799 822
S2 OF REPEAT II (BY SIMILARITY).
TRANSMEM 831 850
S3 OF REPEAT II (BY SIMILARITY).
TRANSMEM 857 876
S4 OF REPEAT II (BY SIMILARITY).
TRANSMEM 893 913
S5 OF REPEAT II (BY SIMILARITY).
TRANSMEM 967 992
S6 OF REPEAT II (BY SIMILARITY).
TRANSMEM 1214 1237
S1 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1251 1276
S2 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1283 1304
S3 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1309 1330
S4 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1350 1377
S5 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1457 1483
S6 OF REPEAT III (BY SIMILARITY).
TRANSMEM 1572 1595
S1 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1602 1625
S2 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1636 1657
S3 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1673 1695
S4 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1721 1786
S5 OF REPEAT IV (BY SIMILARITY).
TRANSMEM 1762 2111
S6 OF REPEAT IV (BY SIMILARITY).
CARBOHYD 211 211
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 284 284
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 295 295
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 301 301
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 306 306
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 338 338
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 601 601
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 621 621
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 681 681
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 892 892
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 1064 1064
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 1080 1080
N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 1146 1146
N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1378 1378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1392 1392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1403 1403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1788 1788 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 875 875 T -> M (IN GEFS+2).
FT VARIANT 1648 1648 /FTId=VAR_010110.
FT VARIANT 1537 1537 R -> H (IN GEFS+2).
FT CONFLICT 1537 1537 /FTId=VAR_010111.
FT CONFLICT 1537 1537 F -> L (IN REF. 3).
SQ SEQUENCE 2009 AA; 228970 MW; 0593A6730F33C9A2 CRC64;

Query Match 49.0%; Score 4496; DB 1; Length 2009;
Best Local Similarity 47.8%; Pred. No. 3.3e-277;
Matches 945; Conservative 287; Mismatches 433; Indels 312; Gaps 38;

Qy 11 PDENRFRPTSDSLAAIKRIAIQERKKSKDKA--AABOPQRPQDLKASRLPKLYGDI 69
Db 11 PDSFNF--FTRESLAAIERIAEAKKPKDPKDDDDENGPKPNSDLEAGNLPFIYDI 68
Qy 70 PPELVTKPLEDLDPYKDKHKTFWLNKRTTYRFSAKRALFILGPNPLRLSMLIRISVHS 129
Db 69 PPEMVSEPLEDLDPYINKTKFIYLNKGAIFRSATSALYILTPFPNPLRKIAIKILVHS 128
Qy 130 VFSMFICTVIINCMMANSMERSFDNDIPEVVFYIGVILBAVTKILARGFIVDFEFLR 189
Db 129 LFSMLIMCTIITNCVFMTPNSPPDWTKV--EYFTGTYTFESLKIARGFCLDFEFLR 187
Qy 190 DPWNWLDIFVIGTAIATCPGSOVNLSALRTRFRVRLKAIASVIGSLYVIGALLRSYK 249
Db 188 DPWNWLDFTVITFAVTEFV--DLGNVSALRTRFRVRLKAIASVIGSLYVIGALLRSYK 246
Qy 250 LVDWVNLTLCLSFALVQQLFMGLNOKCI-----KHNCGPN-----PASN 292
Db 247 LSDVMILTVFCLSFALVQQLFMGLNOKCI-----KHNCGPN-----PASN 292
Qy 293 KDCFEKE-----KDE-----DFTMCGTWLGRPCMGSTCDKTLPLNPDNNYTKFD 338
Db 307 ETVEFDWKS YQDSRYHYFLEGLDALLCGNSSDAGOCPEGYMCVAKRPNNGYTSFD 366
Qy 339 NFGSFLAMFRVWQDSWERLYROILRTSGYIFVFFVFFVFFVFLGSLYLLNLTAVVMY 398
Db 367 TFSWAFSLRLMTQDQWENLYQLTRAAGTKYIMIFFVFLVFLGSLYLLNLTAVVMY 426
Qy 399 EEQNRNVAATEAKEMFOEAQQLLEKE-----ALVAMGIDRS-----438
Db 427 EEQNRNVAATEAKEMFOEAQQLLEKE-----ALVAMGIDRS-----438
Qy 439 -----438
Db 487 SKLSSSAKERRRRKKRQEQSGGEEKDEFEQKSESDSIRKRGPRFSIEGNRLTYE 546
Qy 439 -----SLNSQAASSPKRRFFGSKTRKSF--MRGSKTAQASD-----SED 481
Db 547 KRYSPHOSLIRGSLFSRPR-----NSRSLFSFRGRKADVGSEDFADDEHSTPED 600
Qy 482 DASKNPOL-----LEOTKRLS-----497
Db 601 NESRDSLFVPRRHRGERNSNLSTQSRSRMLAVFPANGKMHSTVDCNGVVSLVGGPSVP 660
Qy 498 -----QNLPLVDLFD-----HV-----DPLHRQALSAVSIL 524
Db 661 TSPVQQLLPEVIDKPAITDNGTTTETEMRRKRRSSSFHVSMDLEDPSPQRQAMSIASIL 720
Qy 525 TITQEQKFOBPCKGNLASKYLVWDCSPQWLCHIKKVLRTITWDPTELATIICIII 584
Db 721 TMTVELESQKCPCCPYKESNIFLWDCSPYWLKVHVYLVNVMDFVDAITICIVL 780
Qy 585 NTVFLAVENHNDNLKTIILKIGWVFTGIFIAEMCLKIIALDPVHYFRHGWNVFDSIVA 644
Db 781 NTLFAMEHYPTWDFNNVLTVGNLVFTGIFTAEMLKIIALMDPPIYFQENIFDGVIV 840
Qy 645 LLSLADV--LYNTLSDNNRSFLASRLVRVFKLAKSWPTLNTLKIIGHSGVAGLNLTVVL 703

841 TLSLVELGLANV---EGLSVLSRSPFLRLRVFKLAKSWPTLNLMLKIIGHSGVAGLNLTVL 897
Qy 704 TIVVIFSVWGMRLFGTKFN---KTAYATQERPRRRHMDNFYHSFLVFRILGGEWIE 759
Db 898 ALIIVFAVGMQLFGSKYKDCVCKIASDCQ---LPRHMDNFYHSFLVFRILGGEWIE 954
Qy 760 NWWGCMQMDGSPCLIIIVFLIWMIGKLVNLFTALLNLSFNEEKDGSLEGETRKTIV 819
Db 955 TMDCM--EVAGQAMCLTVFMVMVIGNLVNLFLALLSLSSFADNL--AATDDDDNEMNL 1012
Qy 820 QLALDRERRAFSFMHLHALQSCCKKRRKNSPKPKEETTESFAGENKOSTLPLDAPKWEY- 878
Db 1013 QIADRMHKGAVYVKKRIYEF-----IOQSF1--RKQILDEIKPLDDLN 1055
Qy 879 ---DTDMALYTOAGAPLAPLAEDDEDDVEYCGEGAL-----PTSOHSA 919
Db 1056 NKDCSMNSHTAEIGKLDYLDKDVNGTTSIGTGSSVEKYIIDESDYMSFINNPSLTVTV 1115
Qy 920 GVOAGDLPPETKQLTSPDOQGVEMEVFSEEDLHLSIQSPRKSDAVSMLSECTIDLNDI 979
Db 1116 PIAYGE-----SDFENLNTEDFSSES---DLEESKEKLNESSESSEGSTVDIGAP 1162
Qy 980 FRNLQKTVSPKK--QPDRCFPKGLSCHFKCHKDRKSPWLVWNIKTCYQIVKHSNPE 1037
Db 1163 VEE--QPVVEPETLEPEACFTGEGVQVQKCCQINVEEGRGQWMLRTRTCFRIVEHNPE 1221
Qy 1038 SFIIIFVILLSSGALIFEDVNLSPRQVBEKLLRCTDNITFTIFLLEMLKMWAFGRFRYFT 1097
Db 1222 TFIIVMILLSSGALAFDIYDQRTIKTMLEYADKVFTYIFILEMLKMWAVGYQYFT 1281
Qy 1098 SAWCHLDPLVVSVLSL-----MNLPSLKSFTLRALRPLRALSOFEGMKVVVYALI 1150
Db 1282 NAWCHLDPLVVSVLSLTANALGYSELGAKSLRTRALRPLRALSFEGRVRYVYVALL 1341
Qy 1151 SAIPAILNVLVCLIFLWVFCILGVNLFSGFRGRCINGT-----DINMYLDFTEPN 1202
Db 1342 GAISIMNVLLVCLIFLWVFCILGVNLFSGFRGRCINGT-----DINMYLDFTEPN 1202
Qy 1203 RSQCINISYWKVQVNFNDVGNAYLALLOVATYKGMLEIMNAAVDSREKQDPDFEALN 1262
Db 1402 RNE-----TARKNVKNVFNVDNFGYLSLLQVATEKGMWDIMYAAVDSRNLVLPQRYEESL 1457
Qy 1263 YAYLVFVFIIFGSPFTLNLFGVIIDNPNQOQKLGODIFMTEEOKKYNNAMKLGTK 1322
Db 1458 YMYLFIIFIGSPFTLNLFGVIIDNPNQOQKLGODIFMTEEOKKYNNAMKLGSK 1517
Qy 1323 KPQKPIRPLNKCQAFVFDLVTISQVFDVILGLIVLNNIIMKASADQPKDKVKTFDILN 1382
Db 1518 KPQKPIRPNKFCQGVFDVTRQVFDISIMILICLNNVMTMVDQSEYVTTILSRIN 1577
Qy 1383 IAFVVIIFIEGLIKVAFALRQHYFTNGWNLFCVQVWVLSIISLTVSRLL--EDSDISPPPLF 1441
Db 1578 LVFIIVFTGECVLKILSRHYFTTGNWIFDFVWVILSVIGMFLAELIEKFVS--PTLF 1635
Qy 1442 RVVRLARIGRILRLVRAARGITLLFALMMSLPSLFNIGLILLFLVMFIYAFGMSWFSKV 1501
Db 1636 RVVRLARIGRILRLKAGRGITLLFALMMSLPSLFNIGLILLFLVMFIYAFGMSWFSKV 1501
Qy 1502 KKGSDIDIFNFTFTGSMCLFIQITTSAGWDTLNLNPMLEAK--EHCN-----SSQDS 1553
Db 1696 KREVIGDDMFNFTFGNMGICLFIQITTSAGWDTLNLNPMLEAK--EHCN-----SSQDS 1553
Qy 1554 CQOQIYAVVYFVYIIISFLIVNMVYIAVLENFNATSEEDPLGEDDFEIFYEWBKF 1613
Db 1756 CGNPSVGIFFFVYIIISFLIVNMVYIAVLENFNATSEEDPLGEDDFEIFYEWBKF 1815
Qy 1614 DPEASQIYQSALSDAFADALPELRVAKPNKFOFLVMDLPVMVMDLHCLMDVLFAPTRV 1673
Db 1816 DPDAQFMEFEKLSQFAALEPPLNLPQNKQLQTLAMDOLPMVSGDRIHCLDLILFAFTKRV 1875
Qy 1674 LGDSSGLDTMTMBEKEKPMANPKKLYEPIVTTTKRKEEGQGAIVIQRAYRKHEK 1730

Db 1876 LCSEGDALRIQMEERFNASNPVKSVQPIITTLTKRQEVSAVIOAIRRHLLK 1932

RESULT 6

CIN3_HUMAN

ID CIN3_HUMAN STANDARD: PRT: 1951 AA.

AC O9NY46: O9Y6PA; Q9UPD1; Q16142; Q9NYK2;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE SODIUM CHANNEL PROTEIN, BRAIN III ALPHA SUBUNIT (VOLTAGE-GATED SODIUM CHANNEL SUBTYPE III).

DE SCH3A OR NAC3.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RP TISSUE=Brain;

RA Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.;

RT "Cloning, distribution and functional analysis of the human brain type III sodium channel from human brain.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-1366 FROM N.A.

RP TISSUE=Brain;

RX MEDLINE=98251277; PubMed=9589372;

RA Lu C.M., Brown G.B.;

RT "Isolation of a human-brain sodium-channel gene encoding two isoforms of the subtype III alpha-subunit.";

RL J. Mol. Neurosci. 10:67-70(1998).

RN [3]

RP SEQUENCE OF 1275-1364 FROM N.A.

RP TISSUE=Placenta;

RX MEDLINE=94211784; PubMed=8159690;

RA Malo M.S., Srivastava K., Andresen J.M., Chen X.N., Korenberg J.R., Ingram V.M.;

RT "Targeted gene walking by low stringency polymerase chain reaction: assignment of a putative human brain sodium channel gene (SCN3A) to chromosome 2q24-31.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).

RN [4]

RP SEQUENCE OF 1620-1701 FROM N.A.

RP TISSUE=Kidney;

RA Tonkovich G.S., Kyle J.W.;

RT "Endogenous sodium current in HEK293 cells: increase in cell surface expression of endogenous currents by stable transfection of the Beta 1 subunit.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch.

CC EMBL; AJ251507; CAB85895.1; -

CC EMBL; AF035685; AAC29514.1; -

CC EMBL; AF035686; AAC29515.1; -

CC EMBL; S69887; AAB30530.1; -

CC EMBL; AF239921; AAF44690.1; -

CC MIM; 182391; -

CC InterPro; IPR002111; Cat_channel_TrpL

CC InterPro; IPR000636; Cation_chan_non_lig

CC InterPro; IPR001682; Channel_pore_Ca_Na

CC InterPro; IPR000048; IQ

CC InterPro; IPR001696; Na_channel

CC Pfam; PF00612; Ion_trans; 4

CC Pfam; PF00612; IQ; 1

CC PRINTS; PR00170; NACHANNEL

CC SMART; SM00015; IQ; 1

CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Multigene family; Alternative splicing.

CC ETCOPROTEIN; Repeat; Multigene family; Alternative splicing.

ET TRANSMEM 124 147 S1 OF REPEAT I.

ET TRANSMEM 156 175 S2 OF REPEAT I.

ET TRANSMEM 189 207 S3 OF REPEAT I.

ET TRANSMEM 214 233 S4 OF REPEAT I.

ET TRANSMEM 249 273 S5 OF REPEAT I.

ET TRANSMEM 401 426 S6 OF REPEAT I.

ET TRANSMEM 706 730 S1 OF REPEAT II.

ET TRANSMEM 742 765 S2 OF REPEAT II.

ET TRANSMEM 774 793 S3 OF REPEAT II.

ET TRANSMEM 800 820 S4 OF REPEAT II.

ET TRANSMEM 836 856 S5 OF REPEAT II.

ET TRANSMEM 910 935 S6 OF REPEAT II.

ET TRANSMEM 1153 1176 S1 OF REPEAT III.

ET TRANSMEM 1190 1215 S2 OF REPEAT III.

ET TRANSMEM 1222 1243 S3 OF REPEAT III.

ET TRANSMEM 1248 1269 S4 OF REPEAT III.

ET TRANSMEM 1289 1310 S5 OF REPEAT III.

ET TRANSMEM 1393 1419 S6 OF REPEAT III.

ET TRANSMEM 1473 1496 S1 OF REPEAT IV.

ET TRANSMEM 1508 1531 S2 OF REPEAT IV.

ET TRANSMEM 1538 1561 S3 OF REPEAT IV.

ET TRANSMEM 1572 1593 S4 OF REPEAT IV.

ET TRANSMEM 1609 1631 S5 OF REPEAT IV.

ET TRANSMEM 1698 1722 S6 OF REPEAT IV.

ET CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 302 302 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 835 835 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 1002 1002 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 1019 1019 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 1317 1317 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CARBOHYD 1331 1331 N-LINKED (GLCNAC. .) (POTENTIAL)

ET CONFLICT 175 175 A -> V (IN REF. 2).

ET CONFLICT 208 208 S -> D (IN REF. 2); AAC29515).

ET CONFLICT 318 318 Y -> N (IN REF. 2).

ET CONFLICT 401 401 M -> T (IN REF. 2).

ET CONFLICT 606 606 S -> T (IN REF. 2).

ET CONFLICT 613 613 V -> E (IN REF. 2).

ET CONFLICT 1011 1011 E -> A (IN REF. 2).

ET CONFLICT 1225 1225 W -> R (IN REF. 2).

ET CONFLICT 1280 1280 V -> L (IN REF. 3).

ET CONFLICT 1365 1366 AT -> VS (IN REF. 2).

SQ SEQUENCE 1951 AA; 221459 MW; B692555143D6C8B5 CRC64;

Query Match 49.0%; Score 4493.5; DB 1; Length 1951;
Best Local Similarity 48.7%; Pred. No. 4.6e-277;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66146901; PubMed=3754035;
RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RT Takahashi H., Numa S.;
RL "Existence of distinct sodium channel messenger RNAs in rat brain.";
Nature 320:188-192(1986).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEABILITY OF EXCITABLE MEMBRANES, ASSUMING OPENED OR CLOSED
CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT.
CC -1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND
2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
EMBL; X03639; CAA27287.1; --
DR PIR; B25019; B25019.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS50096; IQ; 1.
DR Ionic channel; Transmembrane: Ion transport; Voltage-gated channel;
KW Glycoprotein; Repeat; Multigene family.
FT REPEAT 111 456
FT REPEAT 741 1013
FT REPEAT 1190 1504
FT REPEAT 1513 1811
FT TRANSMEM 125 148
FT TRANSMEM 157 176
FT TRANSMEM 190 208
FT TRANSMEM 215 234
FT TRANSMEM 251 274
FT TRANSMEM 402 427
FT TRANSMEM 754 778
FT TRANSMEM 790 813
FT TRANSMEM 822 841
FT TRANSMEM 848 867
FT TRANSMEM 884 904
FT TRANSMEM 958 983
FT TRANSMEM 1204 1227
FT TRANSMEM 1241 1266
FT TRANSMEM 1273 1294
FT TRANSMEM 1299 1320
FT TRANSMEM 1340 1367
FT TRANSMEM 1447 1473
FT TRANSMEM 1527 1550
FT TRANSMEM 1562 1585
FT TRANSMEM 1592 1615

TRANSMEM	1626	1647	S4 OF REPEAT IV.
TRANSMEM	1663	1685	S5 OF REPEAT IV.
TRANSMEM	1752	1776	S6 OF REPEAT IV.
DOMAIN	1905	1934	IQ.
CARBOHYD	212	212	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	285	285	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	291	291	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	303	303	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	308	308	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	340	340	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	604	604	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	624	624	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	883	883	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	1055	1055	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	1072	1072	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	1136	1136	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	1368	1368	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	1382	1382	N-LINKED (GLCNAC. . .) (POTENTIAL)
CARBOHYD	1393	1393	N-LINKED (GLCNAC. . .) (POTENTIAL)
SEQUENCE	2005 AA; 227872 MW; 861BE583D79F8324 CRC64;		

Query Match 48.98; Score 4484.5; DB 1; Length 2005;
Best Local Similarity 48.1%; Pred. No. 1.8e-276;
Matches 950; Conservative 278; Mismatches 448; Indels 301; Gaps 38;

Qy	11	PDERNFRPTSDSLAAIKKRIAIOK-----ERKSKDKAAAEQPPRPOLDLKASRKLPK	64
Dy	9	PGPDSFRFTRESLAAIEQRAEBKAPKQERKDEDD-----ENGKPNLSLEAGKSLPF	64
Qy	65	LYGDIPELVTKPLEDDPYKDKHTFMVLNKRRTIYRFSAKRALFILGPNPLRSLMR	124
Dy	65	IYGDIPPEVSEPLEDDPYINKKTFIVLNKRAISFESATSALYILTPEIRKLAIK	124
Qy	125	ISVHSVSMFTICTVIINCMFMANSERSFNDIPEYVIGIYILEAVIKILARGFIVDE	184
Dy	125	ILVHSLFNLVILMCTILTCNCFMTMSNPPDWTKNV-EYTFGTGYTFESLIKILARGFCLD	183
Qy	185	FSFLRDPNNWLDIFVIGTAIATCPGSOVNLASLRTFFVRALKAKAISVISGLKVTVGALL	244
Dy	184	FTFLRNPNNWLDIFVITFAYVTEFV-NLGNVSALRTFFVLRAKLTISVIPGLKTVIGALI	242
Qy	245	RSVKKLVDVMTLFLCLSFALVGOQLFMGLINOKICKHNGCPNPASN-----	292
Dy	243	QSVKKLSVDMILTVECLSVFALIGLQFMGLNRNKLQW-----PPDNSTEINTTSFN	297
Qy	293	-----KDCFEKEKSEDEIMCGTWLGSRPCPNSTCDKTYT	327
Dy	298	NSLDWNGTAFNRVTNMFNNDEYIEDKSHFYFLEGNDALLCGNSSDAQOCPEGYICVKAG	357
Qy	328	LNPDNNYTKFDNFGWSFLAMFRVMTQDSWERYLQILRTSGIYFVFFVWVIFLGSFYLL	387
Dy	358	RNPNGYTSFDTFSWAFLSLFLRLMTQDPWENLYQTLRAAGKTYMIFVFLVIFLGSFYLI	417
Qy	388	NLTAVTMYAEQNNRVAAETEAKEKMFQE-AQOLLREERKALVAM-----	433
Dy	418	NLILAVVAMAYEEQNQATLEAEQKEAEFQOMLEQLKKQBEAQAAAAAASAESRDFSGA	477
Qy	434	-GIDRSSLNSLOASSFSPPKKRKFPGSKTRK-----	462
Dy	478	GGIGVFSESSSVASKLSKSEKELNRRKKKQREQAGEEBEKEDAVRKSASEDSIRKKG	537
Qy	463	SFEMRGSKTAQ-----ASASDEDD-----	482
Dy	538	QFSEGLSRLTYEKRFSSPHQSLLSIRGSLFSPRRNSRSLNFKGRVKDIDGSENDADDE	597
Qy	483	-----ASKNPQLLEQTKRLSONLPV-----	502
Dy	598	HSTPEDNDSRDSLFVPHRHGERRPSNVYQASRASRGITPLPMNCKMHSAVDCNGVSLV	657
Qy	503	-----DLFDE-----HV-----DPLHQRALSAVSILITITIQ	529

OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92134303; PubMed=1310396;
 RA Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas H.,
 RA Hofmann E.P.;
 RT "Sequence and genomic structure of the human adult skeletal muscle
 RT sodium channel alpha subunit gene on 17q.";
 RL Biochem. Biophys. Res. Commun. 182:794-801(1992).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93338444; PubMed=1339144;
 RA McClatchey A.I., Lin C.S., Wang J., Hoffman E.P., Rojas C.V.,
 RA Gusella J.F.;
 RT "The genomic structure of the human skeletal muscle sodium channel
 RT gene.";
 RL Hum. Mol. Genet. 1:521-521(1992).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=92246457; PubMed=1315496;
 RA George A.L. Jr., Komisarof J., Kallen R.G., Barchi R.L.;
 RT "Primary structure of the adult human skeletal muscle voltage-
 RT dependent sodium channel.";
 RL Ann. Neurol. 31:131-137(1992).
 [4]
 RP VARIANT MET-704.
 RX MEDLINE=92069747; PubMed=1659948;
 RA Ptacek L.J., George A.L. Jr., Griggs R.C., Tawil R., Kallen R.G.,
 RA Barchi R.L., Robertson M., Leppert M.F.;
 RT "Identification of a mutation in the gene causing hyperkalemic
 RT periodic paralysis.";
 RL Cell 67:1021-1027(1991).
 [5]
 RP VARIANT PMC VAL-1592.
 RX MEDLINE=92065978; PubMed=1659668;
 RA Rojas C.V., Wang J., Schwartz L.S., Hoffman E.P., Powell B.R.,
 RA Brown R.H. Jr.;
 RT "A Met-to-Val mutation in the skeletal muscle Na+ channel alpha-
 RT subunit in hyperkalemic periodic paralysis.";
 RL Nature 354:387-389(1991).
 [6]
 RP VARIANTS PMC VAL-1306 AND MET-1313.
 RX MEDLINE=92154689; PubMed=1310898;
 RA McClatchey A.I., van den Berg P., Pericak-Vance M.A., Raskind W.,
 RA Verellen C., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
 RA Brown R.H. Jr., Gusella J.F.;
 RT "Temperature-sensitive mutations in the III-IV cytoplasmic loop
 RT region of the skeletal muscle sodium channel gene in paramyotonia
 RT congenita.";
 RL Cell 68:769-774(1992).
 [7]
 RP VARIANTS PMC PHE-804 AND THR-1156.
 RX MEDLINE=93265141; PubMed=1338909;
 RA McClatchey A.I., McKenna-Yasek D., Cros D., Worthen H.G., Kuncel R.W.,
 RA Desilva S.M., Cornblath D.R., Gusella J.F., Brown R.H. Jr.;
 RT "Novel mutations in families with unusual and variable disorders of
 RT the skeletal muscle sodium channel.";
 RL Nat. Genet. 2:148-152(1992).
 [8]
 RP VARIANTS PMC CYS-1448 AND HIS-1448.
 RX MEDLINE=92265302; PubMed=1316765;
 RA Ptacek L.J., George A.L. Jr., Barchi R.L., Griggs R.C., Riggs J.E.,
 RA Robertson M., Leppert M.F.;
 RT "Mutations in an S4 segment of the adult skeletal muscle sodium
 RT channel cause paramyotonia congenita.";
 RL Neuron 8:891-897(1992).
 [9]
 RP VARIANT PMC ARG-1433.
 RX MEDLINE=93270429; PubMed=8388676;
 RA Ptacek L.J., Gouw L., Kwiecinski H., McManis P., Mendell J.R.,
 RA Barohn R.J., George A.L. Jr., Barchi R.L., Robertson M., Leppert M.F.;
 RT "Sodium channel mutations in paramyotonia congenita and hyperkalemic
 RT periodic paralysis.";
 RL Ann. Neurol. 33:300-307(1993).
 [10]
 RP VARIANTS PMC ALA-1306; GLU-1306 AND VAL-1306.
 RX MEDLINE=94141728; PubMed=8308722;
 RA Lerche H., Heine R., Pika U., George A.L. Jr., Mitrovic N.,
 RA Browatzki M., Welss T., Rivet-Bastide M., Franke C., Lomonaco M.,
 RA Ricker K., Lehmann-Horn F.;
 RT "Human sodium channel myotonia: slowed channel inactivation due to
 RT substitutions for a glycine within the III-IV linker.";
 RL J. Physiol. (Lond) 470:13-22(1993).
 [11]
 RP VARIANT PMC MET-1589.
 RX MEDLINE=94061027; PubMed=8242056;
 RA Heine R., Pika U., Lehmann-Horn F.;
 RT "A novel SCN4A mutation causing myotonia aggravated by cold and
 RT potassium.";
 RL Hum. Mol. Genet. 2:1349-1353(1993).
 [12]
 RP VARIANT PMC ILE-1293.
 RX MEDLINE=96154961; PubMed=8580427;
 RA Koch M.C., Baumbach K., George A.L., Ricker K.;
 RT "Paramyotonia congenita without paralysis on exposure to cold: a novel
 RT mutation in the SCN4A gene (Val1293Ile).";
 RL Neuroreport 6:2001-2004(1995).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
 CC PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT. THIS SODIUM CHANNEL MAY BE PRESENT IN BOTH DENERVATED
 CC AND INNERVATED SKELETAL MUSCLE.
 CC -1- SUBUNIT: MUSCLE SODIUM CHANNELS CONTAIN AN ALPHA SUBUNIT AND A
 CC SMALLER BETA SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
 CC HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
 CC SEGMENT (S4).. SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DISEASE: DEFECTS IN SCN4A ARE THE CAUSE OF BOTH HYPERKALEMIC
 CC PERIODIC PARALYSIS (HYPP) AND PARAMYOTONIA CONGENITA (PMC) WHICH
 CC ARE NOW BOTH KNOWN AS SODIUM CHANNEL DISEASE. CHARACTERIZED BY
 CC MUSCLE STIFFNESS DUE TO MEMBRANE HYPEREXCITABILITY.
 CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
 CC -----
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 CC -----
 DR EMBL; L01983; AAA75557.1; ALT_SEQ.
 DR EMBL; L01962; AAA75557.1; JOINED.
 DR EMBL; L01963; AAA75557.1; JOINED.
 DR EMBL; L01964; AAA75557.1; JOINED.
 DR EMBL; L01965; AAA75557.1; JOINED.
 DR EMBL; L01966; AAA75557.1; JOINED.
 DR EMBL; L01967; AAA75557.1; JOINED.
 DR EMBL; L01968; AAA75557.1; JOINED.
 DR EMBL; L01969; AAA75557.1; JOINED.
 DR EMBL; L01970; AAA75557.1; JOINED.
 DR EMBL; L01971; AAA75557.1; JOINED.
 DR EMBL; L01972; AAA75557.1; JOINED.
 DR EMBL; L01973; AAA75557.1; JOINED.
 DR EMBL; L01974; AAA75557.1; JOINED.
 DR EMBL; L01975; AAA75557.1; JOINED.

DR EMBL; L01976: AAA75557.1; JOINED.
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DR EMBL; L01978: AAA75557.1; JOINED.
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DR EMBL; L01982: AAA75557.1; JOINED.
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DR EMBL; L04231: AAB59624.1; JOINED.
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DR EMBL; L04233: AAB59624.1; JOINED.
DR EMBL; L04234: AAB59624.1; JOINED.
DR EMBL; L04235: AAB59624.1; JOINED.
DR EMBL; M81758: AAB60554.1; JOINED.
DR EMBL; S82622: AAB21450.2; JOINED.
DR PIR; A42099: A42099.
DR PIR; JS0648: JS0648.
DR MIM; 170500: -.
DR MIM; 168300: -.
DR MIM; 168350: -.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Catlon_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS00096; IQ; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Repeat; Multigene family; Phosphorylation;

Query Match 47.4%; Score 4347.5; DB 1; Length 1836;
Best Local Similarity 49.2%; Pred. No. 7.8e-268;
Matches 906; Conservative 272; Mismatches 416; Indels 249; Gaps 35;

Qy 17 RPTFSDSLAAIKKRIATQKERR--KSKDKAAAEQPRQLDLKASRKLPLKLYGDIPPELV 74
Dy 18 RPTFRESLAAEQR-AVEEAEARLORNOQMEIEEPKPRSDLEAGKNLPMYIGDPPPEVI 76
Qy 75 TKPLEDDPYKDHKTVMVANKRTIYFSAKRALFIFGPNPLRSIMRISVHSVFSMF 134
Dy 77 GIPLEDDPYYSNKKTFVILNKAIFAESATPALYLLSPFSVVRGAIKVLIHALFSMF 136
Qy 135 IICVTIINCMPMANSRMSFNDIPEYVIGIYILEAVIKILARGFIVDEFSLRDPNNW 194
Dy 137 IMITILTNCVPMWSDPPWPWSKNV-EYFTGIYTFESLIKILARGFCVDDFTFLRDPNNW 195
Qy 195 LDFVIGTAIATCPGSOVNLISALRTFRVFRALKKAISVISGLKVIYVALLRSVKLLVDVM 254
Dy 196 LDFSVIMMAYLTERV-DLGNISALRTFRVLRALKITIVIPGLKTIYVAGLIQSVKLLSDVM 254
Qy 255 VLTFLCLISFALVGQOFLPMGLINOKIKHNCGPNPASN----- 292
Dy 255 ILTVCLISVFALVGLQFLMGNLROKCVR--WPPPPNDNTWTWYNDTWYGNEM 311
Qy 293 -----KDCFEXE-----KDSEDFIMCGTWLGRPCPN 319

312 WYGNDSVYANDTWNASHASWATNDFDMDAYISDEGNFYFLEGSNDALCNGSNSDAGHCPO 371
320 GSTCDKTTLNPNNNYTKFDNEGWSFLAMFRVMTQDSWRRLYRQLRLTSGIYFVFFVVI 379
372 GYECIKTGRNPNYGYTSYDTFSWAFALFLRLMTQDYWENLQTLTLRAAGKTYMIFVVI 431
380 FLGSFYLLNLFLAVVTMAYEQNRNVAATEAKEMKFOEAQOOLLREEKALVAMGIDRSS 439
432 FLGSFYLLNLFLAVVAMAYABQNEATLAEDKEKEBEEFOOMLEKFKKHOEEL----- 482
440 LNSLQASSFSPPKPKFFGSKTRKFFMRGSKTAQA---SASDESDASKNQOLLEQTKRL 496
483 -----EKAQAALGEAGEADGDPHAGKDCNGSLDTSQG 515
497 SONLPVOLFDEHVDPLHRQRALSAVSILTIITIQEOKEQEPCCPGCKNLASKYLWDCSP 556
516 EKGAP-----RQSGSGDSIGISDAMEELEEAHQKCPWYWKAKHYLIWNCNA 562
557 QWLCIKKVLRTIMTDPFTELAIITIIINTVFLAVEHHMDDNKLTKILKIGNWFTGIFI 616
563 PWLKFKNIHLIVMDPFVDLGTITICIVLNTLFMAHEHPMTEHFDNVLTVGNLFTGIFT 622
617 AEMCLKIILDPYHYFRHGNVFDISIVALLSLADV-LYNTLSNRSFLASLRLVRPKL 675
623 AEMVLKLIAMDPEYFQOGWNIFFDSIIIVTSLVELGLANV---OGLSVLSRFLRLVRPKL 679
676 AKSWPTLNLKIIIGHSVGALGNLTIVIVFISVVGMLRFLGFKENK-TAYATOERPR 734
680 AKSWPTLNLKIIIGNSVGALGNLTIVLAIIVFIVAVGMOQLFGKSYECVCKIALDCNL 739
735 RRWHMDFYHSFLVVRILCGEWIENMMGCMQMDGSPICIIIVFLIMVIGLVVNLFI 794
740 PRWHMDFHSLIVFRILCGEWIETWDCM-EVAGQAMCLTVFLVWVWVNLVNLFI 798
795 ALLNSPSNE-----EKDGSLEGETRKTQVOLADLRFRRAFSF-----MLHALQSICC 842
799 ALLNSFSADSLAASDEDEGM-----NNLQATIGRIKLGIGFAKAFLLGLHG----- 846
843 KRCRRKNSPKPKETESF-----AGENKDSILPDAR--PWKE--YDTDMALYTGOA 889
847 -----KILSPRDIIMLSIGADGAGEGETAPEDKEKPEPDEKKNHILNHHMGLA 900
890 GAP-----LAPLAEVDDVEYCGEGGALPTSQHSAGVQAGLPPET 930
901 DGPSSLELDHLNFINNPYLTIVQPIASESDLE-----MPTEE-----ET 941
931 KOLTSPPDQGVEMEVSEEDLHLSIQSPRKSDAVSMISEGSTIDLDIFRNLKQTV--S 988
942 DTFSEPED-----SKKPPQPLYDGNS--SVCSTADYKPKPEDEPQOABEN 984
989 PK-KOPDRCFKGLSCHFLCHKTOKRSPWVLWNIRKTCYQIVKHSFESFIFVILLS 1047
985 PEGSOPBECFTEACVQRPCLYVDISQGRKKWTLRRACFKIVEHNNFETIFVFMILLS 1044
1048 SGALIFEDVNLSPRQVEKLLRCTDNIFTFLLEMLKLVAFGRFRYFTSAWCWLDLI 1107
1045 SGALAFEDIYIEQRRVIRTILEYADKVTYIFIMELKLVWYAYGKVYFTNAWCWLDLI 1104
1108 VVSVLSLM-----NLPSLKSFTLRALRPLRALSOFEGKVVVYALISAIPAILNV 1160
1105 VDVSTIISLVANMUGYSELGPIKSLRTLALRPLRALSFEGRVVRVVKLLGAIPSMVL 1164
1161 LVCLIFNLVCLIGVLFSGKFGRCINGTDINMYLDTFVFNRSOC-----NISNYSWKP 1216
1165 LVCLIFNLVIFGIMVNLFGAGFYCYITTSERF-DISEVANKSECELSMHTGOVRWLVN 1223
1217 QVNFQNVGNAYLALQVATYKGLWLEIMNAADVSRKDPQDFEALNLYLVFVFIIFGS 1276
1224 KVNVDNVLGYLSLLOVATFKGWDIMVYAAVDSREKEQPOQYEVNLYWLVFIFIIFGS 1283
1277 FFTNLNLTGVTIDNFNQOQKLGQDIFMTEEQKYNAKKLGTKPKQKPTIPRLNKCQ 1336
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Db 1284 FFTLNLFVGIIDNFNQKKLGGKIDFMTBEQKKYYNAMKKLGGKPKQPIPRPQNQIK 1343
Qy 1337 AFVDELVSQVDFVILGILVLNLMIMAESADQPKVKKTFDIL---NIAFVVIFTEC 1393
Db 1344 GWYDLVTKQAFDITIMILICLNMVMTVETDDQS---QLKVDILYNINMIFIIIFTGEC 1400
Qy 1394 LIKVPALRQHYFTNGWNLFCDCVVVLSITISLVSRLESDISFPPTLFRVVLARIGRIL 1453
Db 1401 VKMLALRQHYFTNGWNLFCDCVVVLSITISLVSRLESDISFPPTLFRVVLARIGRIL 1459
Qy 1454 RLVARAGIRTLFALMMSLPSLNFNIGLGLFLVMFIYAFGMSFVKYKGGSGDDIRNF 1513
Db 1460 RLIRAKGIRTLFALMMSLPSLNFNIGLGLFLVMFIYAFGMSFVKYKGGSGDDIRNF 1519
Qy 1514 EFTGSMCLCQITTSAGWDILLNPMLEA-----KEHCNSSQSDSCQPPQTAIVYFV 1565
Db 1520 EFTGSMCLCQITTSAGWDILLNPMLEA-----KEHCNSSQSDSCQPPQTAIVYFV 1579
Qy 1566 SYIIISFLIVVMYIAVILENFNTATESEDPGLGDDFEIYEVNKEKDPASOFIOYSA 1625
Db 1580 SYIIISFLIVVMYIAVILENFNTATESEDPGLGDDFEIYEVNKEKDPASOFIOYSA 1639
Qy 1626 LSFADALPELRLVAKPNKFOFLVMDLPMVMGDRHCHMDVLFAFTTRVLGDSGLDTMKT 1685
Db 1640 LSFADALPELRLVAKPNKFOFLVMDLPMVMGDRHCHMDVLFAFTTRVLGDSGLDTMKT 1699
Qy 1686 MNEKFEANPEKPKLYEPIVITTRKKEEQAANVQRAYRKH 1728
Db 1700 MNEKFEANPEKPKLYEPIVITTRKKEEQAANVQRAYRKH 1742

RESULT 11
CINA_ELEEL
ID CINA_ELEEL STANDARD; PRT; 1820 AA.
AC P02719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE SODIUM CHANNEL PROTEIN (NA+ CHANNEL).
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Gymnotiformes; Electrophoridae; Electrophorus.
OX NCBI_TaxID=8005;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85061498; PubMed=6209577;
RA Noda M., Shimizu S., Tanabe T., Takai T., Kayano T., Ikeda T.,
RA Takahashi H., Nakayama H., Kanaoka Y., Minamino N., Kangawa K.,
RA Matsuo H., Raftery M.A., Hirose T., Inayama S., Hayashida H.,
RA Miyata T., Numa S.;
RT "Primary structure of Electrophorus electricus sodium channel deduced
RT from cDNA sequence.";
RL Nature 312:121-127(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87311395; PubMed=2442385;
RA Noda M., Numa S.;
RT "Structure and function of sodium channel.";
RT J. Recept. Res. 7:467-497(1987).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
CC PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
CC WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
CC HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
CC SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- MISCELLANEOUS: AVAILABLE DATA SUGGEST THAT ACTIVATION AND

INACTIVATION GATES ARE LOCATED NEAR THE CYTOPLASMIC SURFACE OF THE
MEMBRANE. IT IS HYPOTHESIZED THAT RESIDUES 802-806, 847-857,
894-910, AND 942-955 MIGHT, IN CONJUNCTION WITH THE POSITIVELY
CHARGED RESIDUES OF S4, ACT AS A VOLTAGE SENSOR INVOLVED WITH THE
ACTIVATION GATE.
CC -1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
CC
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CC
CC EMBL; X01119; CAA25587.1; -;
CC EMBL; M22252; AAA79960.1; -;
CC PIR; A03178; CHEE.
CC InterPro; IPR002111; Cat_Channel_TrpL.
CC InterPro; IPR000636; Cation_chan_non_lig.
CC InterPro; IPR001682; Channel_pore_Ca_Na.
CC InterPro; IPR001696; Na_channel.
CC Pfam; PF00520; ion_trans; 4.
CC PRINTS; PR00170; NACHANNEL.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Repeat.
CC REPEAT 111 419 I.
CC REPEAT 555 807 II.
CC REPEAT 989 1281 III.
CC REPEAT 1311 1587 IV.
CC TRANSMEM 118 138 S1 OF REPEAT I.
CC TRANSMEM 150 171 S2 OF REPEAT I.
CC TRANSMEM 177 197 S3 OF REPEAT I.
CC TRANSMEM 204 224 S4 OF REPEAT I.
CC TRANSMEM 244 264 S5 OF REPEAT I.
CC DOMAIN 285 342 NON-HOMOLOGOUS REGION OF REPEAT I.
CC TRANSMEM 379 402 S6 OF REPEAT I.
CC TRANSMEM 558 578 S1 OF REPEAT II.
CC TRANSMEM 600 620 S2 OF REPEAT II.
CC TRANSMEM 626 643 S3 OF REPEAT II.
CC TRANSMEM 651 671 S4 OF REPEAT II.
CC TRANSMEM 691 711 S5 OF REPEAT II.
CC TRANSMEM 767 790 S6 OF REPEAT II.
CC TRANSMEM 1005 1025 S1 OF REPEAT III.
CC TRANSMEM 1038 1058 S2 OF REPEAT III.
CC TRANSMEM 1066 1086 S3 OF REPEAT III.
CC TRANSMEM 1092 1112 S4 OF REPEAT III.
CC TRANSMEM 1132 1152 S5 OF REPEAT III.
CC DOMAIN 1172 1194 NON-HOMOLOGOUS REGION OF REPEAT III.
CC TRANSMEM 1244 1264 S6 OF REPEAT III.
CC TRANSMEM 1321 1341 S1 OF REPEAT IV.
CC TRANSMEM 1353 1376 S2 OF REPEAT IV.
CC TRANSMEM 1381 1398 S3 OF REPEAT IV.
CC TRANSMEM 1417 1437 S4 OF REPEAT IV.
CC TRANSMEM 1454 1474 S5 OF REPEAT IV.
CC DOMAIN 1490 1505 NON-HOMOLOGOUS REGION OF REPEAT IV.
CC TRANSMEM 1544 1567 S6 OF REPEAT IV.
CC CARBOHYD 278 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 591 591 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 690 690 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 797 797 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 1160 1160 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 1174 1174 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 1820 AA; 208331 MW; 1B271F626E057864 CRC64;
Query Match 43.4%; Score 3983; DB 1; Length 1820;
Best Local Similarity 46.3%; Pred. No. 1e-244;
Matches 829; Conservative 311; Mismatches 481; Indels 170; Gaps 33;
16 FRPFTSDSLAAIKKRIATQKERRKSKDKAAAEQPRPQLDKSKRLKLYGDIPELV 75

"Two sodium-channel genes in Drosophila: implications for channel diversity.";
Proc. Natl. Acad. Sci. U.S.A. 86:2079-2082(1989).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES, ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: AT LEAST THREE DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PARA GENE.
-1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.

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EMBL: M32078; AAB59195.1; -.
PIR: A32298; A33299.
HSP: P04002; LWFA.
FlyBase: FBgn003036; para.
InterPro: IPR002111; Cat_channel_TrpL.
InterPro: IPR000636; Cation_chan_non_lig.
InterPro: IPR001682; Channel_pore_Ca_Na.
InterPro: IPR001696; Na_channel.
Pfam: PF00520; ion_trans; 4.
PRINTS: PR00170; NACHANNEL.
Kw: Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Alternative splicing; Phosphorylation.
REPEAT 134 467 I.
REPEAT 799 1069 II.
REPEAT 1284 1591 III.
REPEAT 1601 1862 IV.
TRANSMEM 149 172 S1 OF REPEAT I.
TRANSMEM 181 199 S2 OF REPEAT I.
TRANSMEM 213 231 S3 OF REPEAT I.
TRANSMEM 238 257 S4 OF REPEAT I.
TRANSMEM 274 297 S5 OF REPEAT I.
TRANSMEM 406 427 S6 OF REPEAT I.
TRANSMEM 813 837 S1 OF REPEAT II.
TRANSMEM 849 873 S2 OF REPEAT II.
TRANSMEM 881 900 S3 OF REPEAT II.
TRANSMEM 907 926 S4 OF REPEAT II.
TRANSMEM 942 963 S5 OF REPEAT II.
TRANSMEM 1014 1041 S6 OF REPEAT II.
TRANSMEM 1297 1320 S1 OF REPEAT III.
TRANSMEM 1335 1359 S2 OF REPEAT III.
TRANSMEM 1366 1387 S3 OF REPEAT III.
TRANSMEM 1392 1413 S4 OF REPEAT III.
TRANSMEM 1433 1454 S5 OF REPEAT III.
TRANSMEM 1534 1560 S6 OF REPEAT III.
TRANSMEM 1615 1638 S1 OF REPEAT IV.
TRANSMEM 1650 1673 S2 OF REPEAT IV.
TRANSMEM 1680 1703 S3 OF REPEAT IV.
TRANSMEM 1714 1735 S4 OF REPEAT IV.
TRANSMEM 1751 1773 S5 OF REPEAT IV.
TRANSMEM 1836 1860 S6 OF REPEAT IV.
MOD_RES 553 553 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
MOD_RES 570 570 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 325 325 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 682 682 N-LINKED (GLCNAC. .) (POTENTIAL).
FT RT

ET	982	982	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	1055	1055	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	1180	1180	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	1463	1463	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	1492	1492	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	1862	1862	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	2047	2047	N-LINKED (GLCNAC. . .) (POTENTIAL).
ET	555	575	MISSING (IN A SPLICED FORM).
ET	1099	1121	MISSING (IN A SPLICED FORM).
ET	189	189	Y -> C (IN ZS20.2).
ET	198	198	M -> V (IN ZS20.2).
ET	205	205	M -> V (IN ZS20.2).
ET	2131	2131	AA; 239385 MW; D1ECE68845A90F16 CRC64;
SEQ			

Query Match	38.4%;	Score	3524.5;	DB 1;	Length	2131;			
Best Local Similarity	38.1%;	Pred.	No.1.6e-215;						
Matches	784;	Conservative	347;	Mismatches	522;	Indels	407;	Gaps	

QY	9	IFPDERN-FRPFTSDSLAAIKRIATQKERRKSKDAAAE-----	47
DB	8	ISEEERSLFPFTRESLQVEQRIAAEHKEKLEKRAEGEVPYGRKKKOKKEIYDDE	67
QY	48	-----PQRPQLDLKASRKL-----KLYGDIPELVTKPLEDDPYKYDKHKTVMVNLKRT	99
DB	68	DEDEGQDPDTLE-----QGVPIPVRLQGSFPPELASTPLEDDIDPYSNVLTFVVSXGKD	123
QY	100	IVRFSAKRALFILGPNPRLSMIRISVHSVFSMFCTIVINCMPMANSMEKSFNDIP	159
DB	124	IFRSASKAMMLDPNPRIIRVAIYTLVHPLFSLFTITTLVNCILMI-----MPTTPTVEST	181
QY	160	EVFVIGIYILEAVIKILARCFIVDESFLRDPNWNLDLFIQVTAIATCPGSOV-NLSAL	218
DB	182	EVIFTGIYTESAVKVMYKGFILCPPTYLRDAMNWLDFVVIAYVTM--GIDLGNLAAL	239
QY	219	RTFRVERALKATSVISGLVIVGALLRSVKLVDMVWLTLFLCISIFALYGOQLFMGLNQ	278
DB	240	RTFRVLRALKTAIVPGLKTIVGAVIESVKNLRDVILITWFSLSVFMGLQIYMGVLIE	299
QY	279	KCIK-----HNCQPNPASNKDCFEKEKDSDFIMCQTWLGSRPCNG	320
DB	300	KCIKPLPDGSGWNLTDENWDYHN-----RNSNNYSDEGIFSPFLCGNISGAGOCDD	353
QY	321	STC-DKTTLNPNNTYTKDFNGWSFLAMFRVMTQDSWERYLROILTSGIYFVFPFVVVI	379
DB	354	YVCLOGFGPNPNYGYTFSDFSGWAFUSAFRLMTQDFMEDLYQLVLRAAGPWHMLFFVII	413
QY	380	FLGFSYLLNLTLAVTVMAYEQNRNVAAATEAKEKMFQEAQOLL-----	423
DB	414	FLGFSYLVNLLIAIVAMSDELQKAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE	473
QY	424	-----REEKALVAMGIDRSLSN-441	
DB	474	AAAAAAAEAAALHPMAKSPYSCISYELFVGEGKNDNNKESIRSVEVESESVS	533
QY	442	-----SLQASFSPPKRRKFGSKTRKSFPMR-GSKTAQASA	476
DB	534	IQRQAPTTHAQATKVRKYVSTTSLSPGSPFNIR-----GSRSSHKYITRNGRGFGPG	589
QY	477	SDSEDDAKNPOLLEQTKRLNSLNPVDLFDEHVDPL-----	512
DB	590	SD-----RKPLVSTYQAAQHLPPYADDSNAVTPMSEENGAIIVPYVYGNLGSRRHSYT	643
QY	513	-HRQR-----ALSAYSILITITIOFEK-----	533
DB	644	SHQSRISTYSHGDLGGMAVMGVSTWTKESKLRRNTRNQSVCATNGGTTCLDTHKLDH	703
QY	534	-----FQBP-----	538
DB	704	RDYEIGLECTEAGKIKHNDNPFIEPVQOTVVYDMKDVMLNDIIEQAAGRHSRASDRGV	763
QY	539	-----PPC-----GKNLASK-----YLVWDCSPQWILCKVLRTINTDPTELA	577

Db 764 SVYFPTDEDDGPTFKKALEVILKIDVFCVMDCCWMLKFOEWSVLIVDFPVELF 823
Qy 578 ITICIIINTVFLAVEHNMNDNLTKIKGNVFTGIFAEWCKLIKIALDPYHFRHGWN 637
Db 824 ILCIVNTMEMANDHDMKMERVLKSGNYFTATFAIETATKMLAMSPKYVFOEGWN 883
Qy 638 VFDISVALLSLADVLNLTNNNSRFLASRLVRFKLAWSPTLNTLKIIGHSVGALG 697
Db 884 IFDFIIVALSLEGLGV--QGLSVLSRFLRLVFKLAKSWPTLNLISIMGRMTGALG 941
Qy 698 NLTVLTIVVFIESVGMRLFGTF--NKTAYATQTERPRRHHMDNEVHSLVFLVRLCG 755
Db 942 NLTFVLCTIIFIVAMGQLFGKNYHDKORPPDGLD--RWNTDFMHSFIVFVLVCG 999
Qy 756 EWIENMGMCDMGSPICITVFLVIMVIGKLVNLFIALLNSFSNEERDGSLEGETR 815
Db 1000 EWIESMMDCMVGVDS--CIPFLATVIGLVNLFLALLNSNFGS---SSLSAPTA 1053
Qy 816 ---KTKVOLADLRFRAPFSLHALOSFCCCKRKK-----NSPKPKETTE----- 858
Db 1054 DNDTNKIAEAFNRIGREKSWKRIAD--CFKLIRNKLTNQISDQSPGERTNQISWINSEG 1112
Qy 859 ----SFAGENKDSILPDARWKEVYDTDMALYTGQAGAPLAPLAIVEDDVEYCGEGGALP 913
Db 1113 KGVCRCSIAEHGDEL-----ELGHEIDAILDGLIKKEIQOLEVAI-----GDGME 1160
Qy 914 TSQHSAGVQAGDLPETKQLTSPD-----QGVME 944
Db 1161 FTIH--GDMKNKPKSKYLNNATDDTASINSYSHKNRPFKDESHKSGSAETMEGEKR 1218
Qy 945 VFSEDLHLSTQSPRKSDAVMSLSECTIDLN--DIFRNLOKTVPSPKQPRCPKGLSC 1003
Db 1219 DASKEDLGL-----DEELEDGECEEGPLDGDIIHAHDEIDILDEYDACCPCDSYK 1270
Qy 1004 HFLCHKTDKRSPPVLMNIRKTCVOIVKHSWFESIFLVILSSGALIFEDVNLSPRPQ 1063
Db 1271 KFTPLAGDDDDSPFQWGNLRLKFLRLJEDYFATVITMLMSLAUALDEHLVLPQRPI 1330
Qy 1064 VEKLRLCTDNIFTIFLEMLIKWAFGRFRYFTSANCWDLFLIVVSVLSLM----- 1116
Db 1331 LQDILYVMDRIFTVIFLEMLIKLALGKVLVTNACWDLFVIMVSLINFLVSLVAG 1390
Qy 1117 NLPSLKSPRTALRPLRALPSQEGMKVVYVALISAIPAILNVLVLFLVFLVLCILGVN 1176
Db 1391 GIOAFKMTLRLALRPLRAMSGMRVYVVALYQAIPIFNVLVLCILFLIFALIMGVQ 1450
Qy 1177 LFSKFGRC--INGTDINMIDFTEVPRNSOCNISNWKVPQVDFNMGVNAIALLQVA 1234
Db 1451 LFAGKYFKCEDMGTKLSHEI-----IPNRNACESENITWVNSAMDFHGVNAYLCLFOVA 1506
Qy 1235 TYKWLMTMNAVDSREKDEQDFEANYLYFVVFIFGFSFTLNLFIGVITIDNFNQ 1294
Db 1507 TFKGWIQIMDAIDSREVDPKPIRETNIYMYLYFVFIFGFSFTLNLFIGVITIDNFNEQ 1566
Qy 1295 QKLLGGO--DIEMTEOKKYNAWKLGTPKPKQPIPRPLNKCQAFVDFLVTQSVDVIL 1353
Db 1567 KKKAGGSLEMFTEDQKKYISAMKMGSKPLKAIPRWRPQAIIVFVITDKKFDIIM 1626
Qy 1354 GLIVNLIMMAESADQPKDKVKKTFDILNIAFVIFTTECLIKVYFALRQHYFTNGNLF 1413
Db 1627 LFGLNMTMTLDRYDASDTYNAVLDYLAIFVIFSECECLKIFALRYHFIFEPNLF 1686
Qy 1414 CVWVLSIISTLVSR--LEDSDISPPPTLFRVVRVRLARIGRLRLVRAARGIRTLFALMMS 1472
Db 1687 VVWVLSILGLVLSDIEKEVFS--PTLLRVVRVAKVGRVRLVKGAKGIRTLFALMMS 1744
Qy 1473 LPSLFNIGLLFLVNFYIAFGMSWFSKVGSGIDDFENFTGSMCLFQITTSAGW 1532
Db 1745 LPALFNICLLFLVNFYIAFGMSWFSKVGSGIDDFENFTGSMCLFQITTSAGW 1804
Qy 1533 DTLNPLMLEAHCNSSSD--SCQOPQIAVYVYVYIIISFLIVNMYIAVILENF 1587
Db 1805 DGVLDIAIN--EACDPPDNKGYPCNGCGSATVGTITLLSVLIVSFLIVNMYIAVILENF 1863

Qy 1588 NTATESEDPLGEDDFELFYEVWEKFDPEASQFIQYSALSDFADALPEPLRVAKPNKQF 1647
Db 1864 SOATEDVQEGLTDDDDYDMYEIWQOFDEGTQYIRYDQLSSEFLDVLPEPLQIHRKPNKYI 1923
Qy 1648 LVMDLPVYMGDRLLHOMDVLFAFTTRVLGDSGLDMTKMTMEKFMNEANPFKLYEPVIT 1707
Db 1924 ISMDIPICRGDLMYCVDDILDALTKDFFARKG--NPIETGETGEIATAARPDTEGEPVSST 1981
Qy 1708 TKRKEEOGAIVQIRAVRKH 1727
Db 1982 LWOREEYCARLIQHAWRKH 2001

RESULT 13

Clng_HUMAN STANDARD; PRT; 1682 AA.
Q01118; 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM CHANNEL PROTEIN, CARDIAC AND SKELETAL MUSCLE ALPHA-SUBUNIT.
SCN6A.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Heart, and Retal skeletal muscle;
MEDLINE=92279233; PubMed=1317577;
George A.L. Jr., Knittle T.J., Tamkun M.M.;
"Molecular cloning of an atypical voltage-gated sodium channel
expressed in human heart and uterus: evidence for a distinct gene
family".
Proc. Natl. Acad. Sci. U.S.A. 89:4893-4897(1992).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
GRADIENT.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: HEART AND UTERUS.
-1- DOMAIN: THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
EVERY THIRD POSITION.
-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS.
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or send an email to license@isb-sib.ch).
EMBL; M91556; AAA59899.1; -
PIR; A45380; A45380.
MIM; 182392; -
InterPro; IPR000636; Cation_chan_non_lig.
InterPro; IPR001682; Channel_pore_Ca_Na.
InterPro; IPR000048; IQ.
InterPro; IPR001696; Na_channel.
Pfam; PF00520; Ion_trans; 4.
Pfam; PF00612; IQ; 1.
PRINTS; PR00170; NACHANNEL.
SMART; SM00015; IQ; 1.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
Glycoprotein; Repeat; Multigene family; Phosphorylation.
TRANSMEM 114 140
SI OF REPEAT 1 (BY SIMILARITY).

Db 358 OSLKEQERR--NTLTVSEADSHVDORN-----CTCCEQ-----CCGC----- 392
Qy 547 SKYLWDCSPQWLCKIKVLRITMDPTTELATITICIIINTVFLAVEHHNMDNLKI 606
Db 393 -----CYNPMLRVQSFACIIITDSFEVFIIFIVLINTVFLAMEHGMSELKNVLKV 445
Qy 607 GNWFTGFIABMCLIIIALDPYHFRGWNVDISVALLSLADLYLNTLSDNNRSFLAS 666
Db 446 ANYVETTVFVLEAILKLAFAK-QYFKSGWNICDLVVVASLIDLGVEGL--KGVSVFRS 502
Qy 667 LRLRVFKLAKSWPTLNTLIIKIHSGVAGNLATVVLTVVVFVSVGWRFLGTFKNKTA 726
Db 503 FRLRVFHLAQSWTTRMLLIIILTLGLVLTIIILIVIVFAVTGLQLFHTETPTDK 562
Qy 727 YATQERPRRRHMDNFYSFLVPRILCGEWIENWGMCMQMDGSPICIIIVFLIMVIGK 786
Db 563 FRGEVPP--RWNFDLHSMFVPRILCGEWIEPYDCMRACNG--LCFLIFIPVTVFGK 618
Qy 787 LVVLNLFIALILNFSNEKDGSLBGETRKTQVQLALDRFRRAFSLHALQSFCCCKCR 846
Db 619 TLFF-LFGLVLAGSDTVQOEVE-----VSSFALPGPES----- 653
Qy 847 RKNSPKPKETTESFAGENKSDILDPARKEYDTDMALYTOGAGAPLAPLAEVEDDVEYC 906
Db 654 -----KPCSVREGRISATDDNVKDDG-----QDEVQON 681
Qy 907 GEGGALPTSQHSAGVQAGDLPTPK-QLTSPDDQ--GVMEVFSEEDLHLSIQSPRKS 962
Db 682 SE-----ETKIDLRNNDKOSGMILENNCNDNSLASLGS-----L 717
Qy 963 DAVSMLSECSITDLNIPNLQKTVSPKQDPKCPKGLSCHFLCHKDKRKSPPVWLWN 1022
Db 718 GSIPDIMDGSVE-DDISSCQKQIQP-----CLPLFISRFKCLREFDTSHGKKNW 770
Qy 1023 IRKTCYQIVKUSWESFIIFVILLSSGALIFEDVNLPSRQVEKLLRCDNIFTFIFILE 1082
Db 771 FRQLMVCENKPYFTGLVLIIFASSILLAFEDIYLNKPKLAIKFIIDITFCLLFFLE 830
Qy 1083 MLKWAFGFRFYFTSAMCLDFLIVVSVLSLM-----NLPKSKFRTRLRALRPLRA 1135
Db 831 MVKLVALGVHYHFTHTIDFTIIVIVISLAAGLGMQITAFRSLRTRLRALRPLRA 890
Qy 1136 LSQEGMKVYVYALISALIPALINLVLCIFLWVLCILGVNLFSKFGRCINGTDINMYL 1195
Db 891 VSRQGMKIIIVNALMSPISIFNVLVCVFWLFAINGVOLFAKGYKVCNET--NNRI 948
Qy 1196 DTEVPNRSCQNISYKVKVQVFNEDVGNVAYLALLQVATYKGLMEINNAVDSREKDEQ 1255
Db 949 PPTVANKIECYNKNTVWVSNVFNPDVNGGAFALFQVATEFGWMEIMADAVDTEVDEQ 1008
Qy 1256 PDFEANLYLVVYVFIIFGFFTLNLFIVIGVINDFNQOKKLGSO--DIFWTEBOKKY 1313
Db 1009 PKFEATVYVYFVLFIFGFFVNLVIGVINDKFSLKKYDGTYLDMFLTPQOQNY 1068
Qy 1314 NAMKLGTKPKPKPIPRPLNRCQAFVFDLVTSQVDFLVLIGLVLINLMIMMAESADQPKD 1373
Db 1069 NTLKLGTKPKPKQVTKRPNKRCQAVVYDLVMSNQPEIFITITITNMFMAFHYNQSEV 1128
Qy 1374 VKKFDILNIAFVIFTTECLIKVAFALRQHYFTGWNVLFDCVVVLSIISLVSRLSDS 1433
Db 1129 VTEVLATANIAFTIAYAEAIKIIGLRIHLNVLNWNVDFLVTLSYMDAFLNDFDGD 1188
Qy 1434 ISFPTPLFRVRLARIGRILVRAARGIRTLFALMMSLPSLNFNIGLFLVLMFIYAI 1493
Db 1189 IFMNPSSLRVARMEFGRILRIKWKAGMKRLLFALVLSLFAFNIGALLMLVFIYII 1248
Qy 1494 GMSWFSKVGSGIDIPNFTFTGSMCLFQITTSAGWDTLLNPMLEAKHCNSS----- 1549
Db 1249 GMSWFGQIKLGGALNDQVNFQTFGKTFLLVRLATSAGWDLGPELLLPNCDPNYITT 1308
Qy 1550 -----SQDSQCOQPIAVVYFYSYIIISFLIVVNMVIAVLENFNATSESDPLGED 1601
Db 1309 STGEKIKVVGDCGWPWIAISYMYSIIVIFVFNMYIAVLENFNQAHQAEVEGIPED 1368

Qy 1602 DFEIFYEWKEDPEASQFIQYSALSDFADALPEPLRYAKPNKFQFLVMDLPMVMDRLH 1661
Db 1369 DLDMEFYGWEOYDPLATOFIKIHEQUSDFIQDLDPKPKPNNAVAITFDLPVIRGGH 1428
Qy 1662 CMDVLFAFTTRVLG----DSSGLDTMKTMEEKPEANPFKKLYBPVITVTKRKEEQA 1717
Db 1429 CLDILLALVKALGNLEETEAFKRVRTQMEARFDEIFPTREKSEIRISTLQMRREMA 1488
Qy 1718 AVIORYAK 1726
Db 1489 RTLQRAWK 1497

RESULT 15
CCAM_MUSDO
ID CCAM_MUSDO STANDARD: PRT: 1687 AA.
AC Q25452;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1).
CS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Musca.
QC NCBI_TaxID=7370;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Muscle;
PC MEDLINE=94148084; PubMed=8313972;
KA Grabner M., Bachmann A., Rosenthal F., Striessnig J., Schultz C.,
KA Tautz D., Glossmann H.;
RT "Insect calcium channels. Molecular cloning of an alpha 1-subunit from
housefly (Musca domestica) muscle.";
HL FEBS Lett. 339:189-194(1994).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH (BY SIMILARITY). MDL-
ALPHA1 ENCODES A DIHYDROPYRIDINE- AND DILTIAZEM-SENSITIVE CURRENT
IN LARVAL BODY WALL MUSCLE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE LARVAL BODY
WALL MUSCULATURE. IN ADULTS, HIGHEST EXPRESSION IN THORAX FOLLOWED
BY HEAD AND AT A LOWER EXTENT BY ABDOMEN.
CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIE OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; Z31723; CAA83514.1; -;
DR InterPro; IPR002077; Ca_channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.

Search completed: February 27, 2002, 01:39:36
Job time: 635 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2002, 01:28:56 ; Search time 114.56 Seconds
(without alignments)
2253.585 Million cell updates/sec

Title: US-09-646-224A-2

Perfect score: 9173

Sequence: 1 MEERYYPVIFPDERNRPFPT.....VFCNGDLSLDVAKVKVHND 1765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPREMBL_17:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9157	99.8	1765	11 088457	088457 rattus norv
2	8153	88.9	1765	11 09R053	Q9r053 mus musculu
3	8085	88.1	1765	11 09JMD4	Q9jmd4 mus musculu
4	6714	73.2	1791	4 09UI33	Q9ui33 homo sapien
5	6709	73.1	1791	4 09UHE0	Q9uhe0 homo sapien
6	5329	58.1	1444	4 09UHM0	Q9uhm0 homo sapien
7	4730	51.6	2019	11 09JVV9	Q9jvv9 mus musculu
8	4669	50.9	1956	6 09Y5Y9	Q9y5y9 homo sapien
9	4555	49.7	1958	11 P70276	P70276 mus musculu
10	4553	49.6	1956	11 062968	Q62968 rattus norv
11	4553	49.6	1977	4 Q15858	Q15858 homo sapien
12	4545	49.6	1957	11 063554	Q63554 rattus norv
13	4541	49.5	1984	11 008562	Q08562 rattus norv
14	4532	49.4	1962	6 046669	Q46669 canis famil
15	4515	49.2	1984	6 028644	Q28644 oryctolagus
16	4510	49.2	2005	4 09B2D0	Q9bzd0 homo sapien
17	4509	49.2	2005	4 09B2C9	Q9bzc9 homo sapien
18	4489	48.9	1951	4 09B2B3	Q9bzb3 homo sapien
19	4478	48.8	1999	4 09C008	Q9c008 homo sapien

20	4477	48.8	2007	13 09YGN7	09ygn7 cynops pyrr
21	4470	48.7	1951	4 09C007	Q9c007 homo sapien
22	4453	48.5	2000	4 09C006	Q9c006 homo sapien
23	4396	47.9	1978	11 09WTU3	Q9wtu3 mus musculu
24	4394	47.9	1978	11 088420	O88420 rattus norv
25	4390	47.9	1988	11 088421	O88421 rattus norv
26	4381	47.8	1840	11 070611	O70611 rattus norv
27	4380	47.7	1980	4 09UQD0	Q9uqd0 homo sapien
28	4375	47.7	1980	4 095788	O95788 homo sapien
29	4368	47.6	1732	11 060858	O60858 mus musculu
30	4365	47.6	1949	13 09DF53	Q9df53 brachydanio
31	4359	47.5	1841	11 09ER60	Q9er60 mus musculu
32	4354	47.5	1980	4 09NYX2	Q9nyx2 homo sapien
33	4316	47.1	1976	11 063541	O63541 rattus norv
34	4171	45.5	1880	13 09IBF1	O9ibf1 takifugu pa
35	4083	44.5	1834	6 028371	O28371 equus cabal
36	3918	42.7	2049	5 025150	Q25150 halocynthia
37	3833	41.8	1717	13 090519	Q90519 fugu rubrip
38	3554	38.7	2105	5 025439	Q25439 musca domes
39	3554	38.7	2105	5 094615	Q94615 musca domes
40	3550	38.7	2104	5 025440	O25440 musca domes
41	3546	38.7	2031	5 001306	O01306 blattella g
42	3542	38.6	2031	5 001307	O01307 blattella g
43	3541	38.6	2131	5 09VXF7	Q9vxf7 drosophila
44	3535	38.5	2118	5 024531	Q24531 drosophila
45	3530	38.5	2110	5 024532	Q24532 drosophila

ALIGNMENTS

RESULT 1

088457 ID 088457 PRELIMINARY; PRT; 1765 AA.
AC 088457;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VOLTAGE-GATED NA CHANNEL ALPHA SUBUNIT NAN.
GN SNS2.
GS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
GX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;
FX MEDLINE=98338024; PubMed=9671787;
RA Dib-Hajj S.D., Tyrrell L., Black J.A., Waxman S.G.;
RT "NaN, a novel voltage-gated Na channel, is expressed preferentially in peripheral sensory neurons and down-regulated after axotomy."; Proc. Natl. Acad. Sci. U.S.A. 95:8963-8968(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;
RA Tate S.N.;
FL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;
FX MEDLINE=99212311; PubMed=10196578;
RA Tate S.N., Benn S.C., Hick C.A., John V.H.;
RT "Two sodium channels contribute to the TTX-R sodium current in primary sensory neurons."; Nat. Neurosci. 1:653-655(1998).
RN [4]
RP Nat. Neurosci. 1:653-655(1998).
FX EMBL; AF059030; AAC40199.1; .
RA EMBL; AJ237852; CAB41850.1; .
RN [5]
RP InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00520; ion_trans; 4.

DR PRINTS: PR00170; NACHANNEL..
DR PROSITE: PS00120; LIPASE_SBR; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1765 AA; 201843 MW; AE8C67397CC60BD9 CRC64;

Query Match 99.8%; Score 9157; DB 11; Length 1765;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1761; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEERYVPVFPDERFERPFTSDSLAAIKKRIATIAOKERKSKDAAAEQPPRLDLSKASR 60
DB 1 MEERYVPVFPDERFERPFTSDSLAAIEKRIATIAOKERKSKDAAAEQPPRLDLSKASR 60

QY 61 KLPKLYGDIPELVKPKLEDLPYKDKHKTWMLNKKRTIYRFSAKRALFILGPNPLRS 120
DB 61 KLPKLYGDIPELVKPKLEDLPYKDKHKTWMLNKKRTIYRFSAKRALFILGPNPLRS 120

QY 121 LMIRISVSHVSFMFTICTVIINCMPMANSERSFNDIPEYVFIYILEAVIKILARGF 180
DB 121 LMIRISVSHVSFMFTICTVIINCMPMANSERSFNDIPEYVFIYILEAVIKILARGF 180

QY 181 IVDEFSFLRDPNNWLDIVIGTAIATCPGSOVNLALRTRVFRALKASIVISGLKIV 240
DB 181 IVDEFSFLRDPNNWLDIVIGTAIATCPGSOVNLALRTRVFRALKASIVISGLKIV 240

QY 241 GALLRSVKLVDMVLTFLCLISFALVGQQLFMGLNOKICKHNGCPNPASNKDCFEK 300
DB 241 GALLRSVKLVDMVLTFLCLISFALVGQQLFMGLNOKICKHNGCPNPASNKDCFEK 300

QY 301 DSEDIMCGTWLGSRPCNGSTCDKTTLPNNNTYKDFNFGWSFLAMFRVMTQDSWERLY 360
DB 301 DSEDIMCGTWLGSRPCNGSTCDKTTLPNNNTYKDFNFGWSFLAMFRVMTQDSWERLY 360

QY 361 ROLLRTSGIYFVFPVVFVIFGSLVLLNLTAVVTMAYEQNRNVAATEAKEKMFQBAQ 420
DB 361 ROLLRTSGIYFVFPVVFVIFGSLVLLNLTAVVTMAYEQNRNVAATEAKEKMFQBAQ 420

QY 421 QLLREKEALVAMGIDRSLSLQASFSPPKRRKFFGSKTRKSPMRGSKTAQASADSE 480
DB 421 QLLREKEALVAMGIDRSLSLQASFSPPKRRKFFGSKTRKSPMRGSKTAQASADSE 480

QY 481 DDASKNPOLLGQTKRLSONLPVDLDEHVDPLHQRALSAVSILTIITQEQEKFOEPCFP 540
DB 481 DDASKNPOLLGQTKRLSONLPVDLDEHVDPLHQRALSAVSILTIITQEQEKFOEPCFP 540

QY 541 CGKNLASKYLWDCSPQWLCIKKVLRTIMTDPFTTELATITICIIINTVFLAVEHHNMDNL 600
DB 541 CGKNLASKYLWDCSPQWLCIKKVLRTIMTDPFTTELATITICIIINTVFLAVEHHNMDNL 600

QY 601 KTLKIGNWVFTGIFIAEMCLKIITADLPYHFRHGNVFNDSIVALLSLADLYLNTLSNN 660
DB 601 KTLKIGNWVFTGIFIAEMCLKIITADLPYHFRHGNVFNDSIVALLSLADLYLNTLSNN 660

QY 661 RSFLASRLVRVKLAKSWPTLNTLIKTIHSGVAGLNLTVLTVTFVIFSVGMRLFGT 720
DB 661 RSFLASRLVRVKLAKSWPTLNTLIKTIHSGVAGLNLTVLTVTFVIFSVGMRLFGT 720

QY 721 KFNKTAYATQERPRRRWHDNFYHSFLVFRILCGEWIENMGCMQMDGSPLCIIVFL 780
DB 721 KFNKTAYATQERPRRRWHDNFYHSFLVFRILCGEWIENMGCMQMDGSPLCIIVFL 780

QY 781 IMWIGKLVNLFITALLNSFSNEKDGSEGTERTKTKVQLALDRFRRAFSEFMLHALQSF 840
DB 781 IMWIGKLVNLFITALLNSFSNEKDGSEGTERTKTKVQLALDRFRRAFSEFMLHALQSF 840

QY 841 CCKKRRKNSPKPKETTESFAGENKDSILPDARPKWEYDMDALYTGQAGAPLAPAEVE 900
DB 841 CCKKRRKNSPKPKETTESFAGENKDSILPDARPKWEYDMDALYTGQAGAPLAPAEVE 900

QY 901 DDVEYGGGALPTSQHSAGVQAGDLPPETKQLTSPDQGVEMEVFSEEDLHLISQSPRK 960
DB 901 DDVEYGGGALPTSQHSAGVQAGDLPPETKQLTSPDQGVEMEVFSEEDLHLISQSPRK 960

RESULT 2

Q9R053 PRELIMINARY; PRT; 1765 AA.
AC Q9R053;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL NAN.
CN SCN1IA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
EN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.

RESULT 3
Q9JMD4 PRELIMINARY; PRT: 1765 AA.
ID Q9JMD4
AC Q9JMD4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created).
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT NAT/SCN1A.
GN SCN1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20090627; PubMed=10623609;
RA Ogata K., Jeong S.Y., Murakami H., Hashida H., Suzuki T., Masuda N.,
RA Hirai M., Ishihara K., Uchiyama Y., Goto J., Kanazawa I.;
RT "Cloning and expression study of the mouse tetrodotoxin-resistant
RT voltage-gated sodium channel alpha subunit Nat/Scn1a.";
RL Biochem. Biophys. Res. Commun. 267:271-277 (2000).
DR EMBL; AB031389; BAA92154.1; -;
DR MG: MG1:1345149; Scn1a.
DR InterPro: IPR000636; Cation_chan_non_lig.
DR InterPro: IPR002111; Cat_channel_Trtpl.
DR InterPro: IPR001682; Channel_pore_Ca_Na.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR001696; Na_channel.
DR Pfam: PF00520; Ion_trans; 4.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1765 AA; 201305 MW; FFF1D121CB9C6DA CRC64;

Query Match 88.1%; Score 8085; DB 11; Length 1765;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1560; Conservative 95; Mismatches 107; Indels 6; Gaps 5;
Qy 1 MEERYYPVFPDERNFRFTSDSLAAIKKRIATIAQKERRKSKDKAAAEQPPRPQLDLKASR 60
Db 1 MEERYYPVFPDERNFRFTSDSLAAIEKRITIOKEKKKSKDKAAATEQPPRPQLDLKASR 60
Qy 61 KLPKLYGDIPPELVTKPLEDDPYKHDKTFWLNKKTTFYFSAKRALFILGPNPLRS 120
Db 61 KLPKLYGDVPPDLAKPLEDDPPYKHDKTFWLNKKTTFYFSAKRALFILGPNPLRS 120
Qy 121 LMIRISHSVSMFICTVIINCMFMAN--SWERSFONDIDPEYFYGIIILEAVIKILAR 178
Db 121 FMIRISHSVSMFICTVIINCMFMANSSVDSPPSNIDPEYFYGIIIVLEAVIKILAR 180
Qy 179 GFIVDEFSFLRDPNNWLDVIFVIGTAIATCFPGSQV-NLSALRTFRVFRALKAISVISGLK 237
Db 181 GFIVDEFSYLRDPNNWLDVIFVIGTAIAPCFLGNKYNLSTLRTFRVLRALKAISVISGLK 240
Qy 238 VIVGALLRSVKLVDMVMTLFLCISIFALVGOQLFMGLLNKCKIKHNCPPNASKDCFE 297
Db 241 VIVGALLRSVKLVDMVMTLFLCISIFALVGOQLFMGLLSQCKIKDDCGPNFASKDCFE 300
Qy 298 KEKSEDFIMCGTWLGRPCPNSTCDKTTLNPDNNYTKFDFNFGWSFLAMFRVMTQDSWE 357
Db 301 KENSEDFIMCGNWLGRSCPDGCTCKTTNPDYNTNFDFSGWSFLAMFRVMTQDSWE 360
Qy 358 RLYRQILRTSGIYFVFVFFVIFGSLFYLLNLTAVTMYAEQNNRNVAATEAKEKMFQ 417
Db 361 KLYRQILRTSGIYFVFVFFVIFGSLFYLLNLTAVTMYAEQNNRNVAATEAKEKMFQ 420
Qy 418 EAQQLLREKEALVAMGIDRSLSLQASSFSPPKRRKFFGSKTRKSPFMRGSKTAQASAS 477
Db 421 EAQQLLREKEALVAMGIDRTSLSLQASSFSPPKRRKFFGSKTRKSPFMRGSKTARASAS 480
Qy 478 DSEDDASKNPOLLEQTKRLSQNLPVDFDEHVDPLHQRALSAVSILTTITIQEQEKFOEP 537

481 DSEDDASKNPOLLEQTKRLSQNLPVDFDEHVDPLHQRALSAVSILTTITIQEQEKSOEP 540
Qy 538 CFPCKGNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTETALITICIIINTVFIAVEHHND 597
Db 541 CFPCKGNLASKYLVWDCSPQWLCIKKVLRTIMTDPFTETALITICIIINTVFIAVEHHND 600
Qy 598 DNLKTLIKGNVFTGIFIAECLKIIAIDDPHYHRHGNVPDSIVALLSLADLYNLIS 657
Db 601 NSLKDILKGNVFTGIFIAECLKIIAIDDPHYHRHGNVPDSIVALLSLADLYNLIS 660
Qy 658 DNNRSFLASLRVLRVFKLAKSNPTLNTLIKIIHGSVGALNLTVVLTIVVFISVVGML 717
Db 661 -KNLSFLASLRVLRVFKLAKSNPTLNTLIKIIHGSVGALNLTVVLTIVVFISVVGML 719
Qy 718 FGTFENKATAYATQERPRRRHMDNFYHSFLVVFRILCGEWENMMGCMQDMGSPCLCIV 777
Db 720 FGAKFNKCTSPESLRRR-HMGDFYHSFLVVFRILCGEWETWMDCHQEMEGSPCLCIV 778
Qy 778 FVLINVIKLVNLFIALLNSFSNEEKDGSLEGETRKTQVQLALDRFRRAFSMLHAL 837
Db 779 FVLINVIKLVNLFIALLNSFSNEEKDGNPEGETRKTQVQLALDRFRSRAFYEMARAL 838
Qy 838 QSFCKCKRRKNSPKPKETTESFAGENKDSILPDARPKNEYDTDMALYTGQAGAPLAPLA 897
Db 839 QNFCRKRRCRRQNSPKPNEATESFAGESRDTATLDRSNKEYDSEMTLYTGQAGAPLAPLA 898
Qy 898 EVEDDVEYCGEGGALPTSOHSAGVQAGDLPPETKQLTSPDDQGVEMEVSEEDLHLSIQS 957
Db 899 KEEDDMCECCGCDASPTSQPSEEAQACDLPLKTKRLSPDDHGVEMEVSEEDPNLTIQS 958
Qy 958 PRKKSDAVSMISECSTIDLNDIFRNLOKTVSPKQDPDRCFPKGLSCHFLCHTKRKSFPW 1017
Db 959 ARKKSDAASMLSECSTIDLNDIFRNLOKTVSPKQDPDRCFPKGLSCIFLCCKTIKKKSPW 1018
Qy 1018 VLWNIRKTCYQIVKHSWFESFIFVILLSSGALLFEDVNLPSRPQVEKLLRCTONITFF 1077
Db 1019 VLWNIRKTCYQIVKHSWFESFIFVILLSSGALLFEDVNLPSRPQVEKLLRCTONITFF 1078
Qy 1078 IFLEMLILKLVAFGRYFTSAWCWLDLFIIVVSVLSLMLNPSLSKSFRTLRALRPLALS 1137
Db 1079 IFLEMLILKLVAFGRYFTSAWCWLDLFIIVVSVLSLMLNPSLSKSFRTLRALRPLALS 1138
Qy 1138 QFEGMKVVYALISAIPAILNVLVCLIFWLVFCILGVNLFSKFGKFCINGTDINMYLDF 1197
Db 1139 QFEGMKVVYALISAIPAILNVLVCLIFWLVFCILGVNLFSKFGKFCINGTDINMYLDF 1198
Qy 1198 TEVNRSCNISNYSWKVPQVNFQVNGNAYLALQVATYKGLWETMNAVDSREKDEQPD 1257
Db 1199 SNVPNQSCLVSNHTWKVPVNFQVNGNAYLALQVATYKGLWETMNAVDSRGDEQPA 1258
Qy 1258 FEANLYAYLVFVFTIFGSEFTNLNFIQVIIDNFNQOKKLGQDIFMTEQKKYYNAMK 1317
Db 1259 FEANLYAYLVFVFTIFGSEFTNLNFIQVIIDNFNQOKKLGQDIFMTEQKKYYNAMK 1318
Qy 1318 KLGTKKPKPPIPRPLNKCOAFVFDLVTQVFDVILGLILVNLMIIMMAESADQPKDKKT 1377
Db 1319 KLGTKKPKPPIPRPLNKCOAFVFDLVTQVFDVILGLILVNLMIIMMAESADQPKDKKT 1378
Qy 1378 FDILNIAFWFTTECLIKVFALROHYFTNGWNLFDVNVVLSIISTLVSRLEDDISGFP 1437
Db 1379 FDILNIAFWFTTECLIKVFALROHYFTNGWNLFDVNVVLSIISTLVSRLEDDISGFP 1437
Qy 1438 PTLFRVRLARIGRLRLVRAARGTIRLLFALMMSLPSLFNLGLLLFLVMFYIAFGMSW 1497
Db 1438 PTLFRVRLARIGRLRLVRAARGTIRLLFALMMSLPSLFNLGLLLFLVMFYIAFGMSW 1497
Qy 1498 FSKVKGSGIDDIENFETFTGSMCLCFQITTSAGHDITLLNPMLEAKEHCNSSSSQSCOP 1557
Db 1498 FSKVKGSGIDDIENFETFTGSMCLCFQITTSAGHDITLLNPMLEAKEHCNSSSSQSCOP 1557
Qy 1558 QIAYVYFYSYIIISPLIVNMVYIAVILENFNTATSESDPLGEDDFEFYFVWEKFDPEA 1617
Db 1558 QIAYVYFYSYIIISPLIVNMVYIAVILENFNTATSESDPLGEDDFEFYFVWEKFDPEA 1617

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Db 1558 QIAIYVFSYIIISLLIIVNMIAVILENFNTATSESDPLGEDDFEIPYIEIWEKFDREA 1617
Qy 1618 SOFIQYSALSDFADALPEPLRVAKPNKQFQFLVMDLPVMVMDGRHLCMDVLFAPFTTRVLGDS 1677
Db 1618 TOFIQYSLSDFADALPEPLRVAKPNKQFQFLVMDLPVMVMDGRHLCMDVLFAPFTTRVLGDS 1677
Qy 1678 SGLDTMKMMEKEKFEANPFKLYEPIVTTTKRKEEBEAGAAVIOQARYAKHMEKWKVLRK 1737
Db 1678 SGLDTMKMMEKEKFEANPFKLYEPIVTTTKRKEEBEAGAAVIOQARYAKHMEKWKVLRK 1737
Qy 1738 DRSSSSHOFVFCNGDLSLSDVAKVKVHND 1765
Db 1738 GRSSSLQVFCNGDLSLSDVPAIKVHCD 1765

RESULT 4
Q9UI33 PRELIMINARY; PRT: 1791 AA.
AC Q9UI33;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT SCN12A.
GN SCN12A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=20090626; PubMed=10623608;
RA Jeong S.-Y., Goto J., Hashida H., Suzuki T., Ogata K., Masuda M.,
RA Hirai M., Isahara K., Uchiyama Y., Kanazawa I.;
RT "Identification of a novel human voltage-gated sodium channel alpha
RT subunit gene, SCN12A.";
RL Biochem. Biophys. Res. Commun. 267:262-270(2000).
DR EMBL; AF109737; AAF24976.1;
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1791 AA; 204947 MW; E85D3E790E141D68 CRC64;
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Query Match 73.2%; Score 6714; DB 4; Length 1791;
Best Local Similarity 72.9%; Pred. No. 0;
Matches 1316; Conservative 178; Mismatches 258; Indels 52; Gaps 14;
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Qy 1 MEERYVPVFPDERNFRFTSDSLAAIKRTAIQKERKSKDKAAAEQPPRLDLKASR 60
Db 1 MDDRCYVFPDERNFRFTSDSLAAIEKRTAIQKERKSKDKQDQGEVPPRLDLKASR 60
Qy 61 KLPLKYGDIPLPLVTKPLEDDIPYKDKHTFMVLNKKRTIYRFSAKRALFILGPPNPLRS 120
Db 61 KLPLKYGDIPLRELICKPLEDDLPFRNKHKTFMVLNKKRTIYRFSAKHALFIFGPPNSIRS 120
Qy 121 LMIRISVHSVSMFICTVIINCMPMANSMER--SFNDPIPEYVFIGIYILEAVIKILA 177
Db 121 LAIRYSVHLSFMFIIGVINCVPMATGPAKNSNSNTDIAECVFTGIYIFEALIKILA 180
Qy 178 RGFVDESFRLDPWNWLDVIFVIGTAIATCPGSOVNLSALRTRFRFRALKAISVISGLK 237
Db 181 RGFILDESFRLDPWNWLDVIGIAIVSIPGITIKLLPLTRFRFRALKAISVISRLK 240
Qy 238 VIVGALLRSVKLVDMVLTFLCISIFALYGOOLPMGLNOKCIKHNCG--PNPASNKDC 295
Db 241 VIVGALLRSVKLVNVIITFLFCSIFALVGOOLPMGLNOKCIKHNCG--PNPASNKDC 300
Qy 296 FEKEKDSDFIMCGTWLGRPCPCNGSTCDKTTLPNDNNYTKRFDNFGWSFLAMFRVMTQDS 355
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Db 301 FEKENSPEFKMCGIMWGNCSACSIQYECKHTKINDYNTNFDNFGWSFLAMFRVMTQDS 360
Qy 356 WERLYRQILRTSGIYVFFVFFVIFLGSFYLLNLAVVTMAYEQNRNVAETAKEMK 415
Db 361 WEKLYQOILRTTGLSVFFVIFLGSFYLLNLAVVTMAYEQNRNVAETAKEMK 420
Qy 416 FOEAQOQLREKEALVAMGIDRSSLSLQASSFSFKRFFGSKTRKFFFMGRGSTAQAS 475
Db 421 FOEAQOQLREKEALVAMGIDRSSLSLQASSFSFKRFFGSKTRKFFFMGRGSTAQAS 480
Qy 476 ASDDEDDASKNPOLLEOTKRLSONLPVDFLDEHVDPLHQRALSAVSILTIITIQOEKQ 535
Db 481 GSDSDEDCQKPOLLEOTKRLSONLSLQASSFSFKRFFGSKTRKFFFMGRGSTAQAS 540
Qy 536 EPCFFCGKNLASKYLWDCSPOWLCTIKKVLRTIMTDPTELTATITCIINTVFLAVEHNN 595
Db 541 EPCLPCCGENLASKYLWNCPPOWLCKVKVLRVMTDPTELTATITCIINTVFLAVEHNN 600
Qy 596 MDDNLKTLIKIGNMVFTGIFIAEMCLKIADLPYHYFRHGMNVFSDISVALLSLADLYNT 655
Db 601 MEASFEKMLNIGNLVFTSIFIAEMCLKIADLPYHYFRHGMNVFSDISVALLSFADVMNCV 660
Qy 656 LSDNRSFLASLVRVLFKLSKSWPTLNTLIKIIGHSVAGLGNLTVLTVIVVIFSVVGM 715
Db 661 LQKRSWPLRSRVLRFKLSKSWPTLNTLIKIIGSVAGLGNLTVLTVIVVIFSVVGM 720
Qy 716 RLFGTKENKATAYATQERPR-----RRWMDNPFYHSFLVVFRTLCGGEWLENMVG 763
Db 721 QLFGRSFN-----SOKSPKLCNPTGTVSCLRHWMGDFWHSLVVFRTLCGGEWLENMVE 775
Qy 764 CMQDMD-GSPLCIIIVFLIMVIGKLVNLFALLNLSFNEEKDGLSEGETRKTQVOLA 822
Db 776 CMQEANASSSLCIVIFLITVIGKLVNLFALLNLSFNEERNGNLSEGEARTKQVOLA 835
Qy 823 LDRFRRAFSLMALQSCCKKCRKNKSPKPKETTESFAGENKDSLTP---DARPMKEYD 879
Db 836 LDRFRRAFCFVRHTLEHFCWKCRKQNLPOKEVAGGCAQAQSKD-IIPVLMEMKRGSEFQ 894
Qy 880 TDMALYTGQAGAP-----LAPLAEVDEDDVEYCEGCGALPTISOHSAGVQAGDLP 928
Db 895 EELGILT---SVPKTLGVNHDWTLAPLAEEDDDVEFGSDGNAQRITQPEPQQAELHQ 951
Qy 929 ETQKLTSPDDQGVEMEVFSEEDLHLSIQSPRKSDAVSMLSECSTIDLNDIFRNKQTVS 988
Db 952 ENKKTQSQRVQSVDEIDMFSEDEPHLTIQDPRKSDVTSILSECSTIDLQDGGNLEPMV 1010
Qy 989 PKKQDPRCPKGLSCHFLCHKTKDKRKSPVLWNNIRKTCYQIVKHSWFESFIIFVILLSS 1048
Db 1011 PKKQPERCLPKGFCGFCPCSVDRKKRPWVWNNLRKTCYQIVKHSWFESFIIFVILLSS 1070
Qy 1049 GALIFEDVNLPSRPOVEKLLRCTDNITFTIFILEMLKWAAGFRFRYFISACWLDLFLV 1108
Db 1071 GALIFEDVHLENQKIQIENLCTDIIFTHIFILEMLKWAAGFRFRYFISACWLDLFLV 1130
Qy 1109 VVSVLSLNLPSLKFRTLRALRALSOFGCMKVYVVALISAIPAILNVLVLCIFWL 1168
Db 1131 IVSVTTLNLMLKELSFRTLRALRALSOFGCMKVYVVALISAIPAILNVLVLCIFWL 1190
Qy 1169 VFCILGNLFSKGFRCINGTDINMYLDFTEVFNRSQCNISNYSWKVPQVNDVGNAYL 1228
Db 1191 VFCILGVYFSGKFCGKINGTD--SVINYTIITNSQCESGNFSWINOKVNDVGNAYL 1248
Qy 1229 ALLQVATYKGLWEINNAVDSREKQDQDFEANLYAYLVFVYVFIIFGSEFTNLNLFIVII 1288
Db 1249 ALLQVATYKGMWDIIIAVADVSTEKQEQPEFESNSLGYIYFVYVFIIFGSEFTNLNLFIVII 1308
Qy 1289 DNFNQOQKLGQDIFMTEEQKYYNAMKLGTKPKQKIPRPLANKCAQAFVLDVTSQVF 1348
Db 1309 DNFNQOQKLGQDIFMTEEQKYYNAMKLGSKKPKQKIPRPLANKCOGLVFDIVTSQIF 1368
Qy 1349 DVIILGLVNLNMIIMMAESADQPKDKKTDILNTIAFVIFVIFTECLIKVFLARQHYFTNG 1408
```

Db 1369 DIIIIISLIILNISMMAESYNOPKAMKSILDLNWNVVFVFTLECLIKIFALRQYVFTNG 1428
QY 1409 WNLFCVWVVLSTIIVLSRLSDS- ISFPPTLFRVRLARIGRILRLVRAARGIRTLIF 1467
Db 1429 WNLFCVWVVLSTIIVLSRLSDS- ISFPPTLFRVRLARIGRILRLVRAARGIRTLIF 1488
QY 1468 ALMMSLPSLFGNGLLFLVMTYIAFGMSWFKVKGSGIDIDIFNFETPGSMCLCFQIT 1527
Db 1489 ALMMSLPSLFGNGLLFLVMTYIAFGMSWFKVKGSGIDIDIFNFETPGSMCLCFQIS 1548
QY 1528 TSAGWDTLLNPMLEAKHCNSQSDCOQPIAVYFVSYIIISFLIVVNMVIAVILENF 1587
Db 1549 TSAGWDTLLNPMLEAKHCNSQSDCOQPIAVYFVSYIIISFLIVVNMVIAVILENF 1607
QY 1588 NTATESEDPGLCEDDFEYEWKFPDEASOFIOYSALSDPADALPEPLRVAKPNKQF 1647
Db 1608 NTATESEDPGLCEDDFEYEWKFPDEATOFIKYSALSDPADALPEPLRVAKPNKQF 1667
QY 1648 LVMDLPVMGDRHLHGMVLFVFTTRVLGDSGLDTMTKMTWEEKFMEANPFKKLYPIVTT 1707
Db 1668 LVMDLPVMGDRHLHGMVLFVFTTRVLGDSGLDTMTKMTWEEKFMEANPFKKLYPIVTT 1727
QY 1708 TKRKEEERGAALIQAFKRYMMKVTKGQDQDNDLNGPHSPLOTLNGLDSSFGVAKG 1761
Db 1728 TKRKEEERGAALIQAFKRYMMKVTKGQDQDNDLNGPHSPLOTLNGLDSSFGVAKG 1787
QY 1762 VHND 1765
Db 1788 VHCD 1791

RESULT 5
QYUHEO PRELIMINARY; PRT; 1791 AA.
ID QYUHEO;
AC QYUHEO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL TYPE XI ALPHA SUBUNIT.
GN SCN1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DORSAL ROOT GANGLIA;
RX MEDLINE=20047838; PubMed=10580103;
RA Dib-Hajj S.D., Tyrrell L., Cummins T.R., Black J.A., Wood P.M.,
RA Waxman S.G.;
RT "Two tetrodotoxin-resistant sodium channels in human dorsal root
ganglion neurons";
RL FEBS Lett. 462:117-120(1999).
DR EMBL; AF188679; AAF17480.1; -.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1791 AA; 204920 MW; DE38680BFB639ED1 CRC64;

Query Match 73.1%; Score 6709; DB 4; Length 1791;
Best Local Similarity 72.9%; Pred. No. 0;
Matches 1315; Conservative 179; Mismatches 258; Indels 52; Gaps 14;
QY 1 MEERYYPVIFPDNERFRFTSDSLAAIKKRTAIQKERRKSKDKAAAPQPRQDLKASR 60
Db 1 MDDRCYPVIFPDNERFRFTSDSLAAIKKRTAIQKERRKSKDKOTGEVQPRQDLKASR 60
QY 61 KLPKLYGDIPPELVTKPLEDDPYKDKHKTFLMVLNKKRTIYRFSAKRALFILGPPFNPLRS 120

Db 61 KLPKLYGDIPPELVTKPLEDDPYKDKHKTFLMVLNKKRTIYRFSAKRALFILGPPFNPLRS 120
QY 121 LMRISVHSVFMFICTVIINCMEMANSMER---SFDNDIPEYFVIGIYILAVIKILA 177
Db 121 LAIRSVHSLFWMFICTVIINCMEMANSMER---SFDNDIPEYFVIGIYILAVIKILA 180
QY 178 RGFIVDESFLLDPNWLDFVIGTAIATCFPGSQVNLALRTFRFRALKAISVISGLK 237
Db 181 RGFILDEFSLDPNWLDSVIGTAIVSYIPGIIKLLPLTRFRFRALKAISVISRLK 240
QY 238 VTVGALLRSVKLVDMVLTFLCLSFALVGOLFPGILNOKCIKHNCG--PNPASNKDC 295
Db 241 VTVGALLRSVKLVNVIILTFCLSFALVGOLFPGILNOKCIKHNCG--PNPASNKDC 300
QY 296 FEKEDSEDFIMCGTWLGRPCNGSTCDKTTLPNDNNYTKFDNFGWSEFLAMFRVMTQDS 355
Db 301 FEKENSPEFKMCGIWMGNSACSIQYCKHTKINPDYNTNFDNFGWSEFLAMFRVMTQDS 360
QY 356 WERLYRQILRTSGIYFVFFVVLGSPYLLNLTLAVTVMAYEQNRNVAATEAKEKM 415
Db 361 WEKLYQOTLRTTGLYSVFFIIVIFLGSFYLLNLTLAVTVMAYEQNRNVAATEAKEKM 420
QY 416 FOEAQOLLREKEALVAMGIDRSSLSLQASSFPKRRKFFGSKTRKSFMRGSKTAQAS 475
Db 421 FOEAQOLLREKEALVAMGIDRSSLSLQASSFPKRRKFFGSKTRKSFMRGSKTAQAS 480
QY 476 ASDDEDDASKNPOLLEQTKRLSONLPVLDLFDHVDPLHQRALSASVILTIQBOEKFO 535
Db 481 GSDSDCQKPKQLLEQTKRLSONLPVLDLFDHVDPLHQRALSASVILTIQBOEKFO 540
QY 536 EPCFPGKNLASKYLWDCSPQWLCKIKVLRITMDPTTELATITCIINTVFLAVEHIN 595
Db 541 EPCFPGKNLASKYLWDCSPQWLCKIKVLRITMDPTTELATITCIINTVFLAVEHIN 600
QY 596 MDDNLTKILIGNWVFTGIFIAEMCLKIITADLPYHFRGNVNFDSIVALLSLADLYNT 655
Db 601 MEASFEMKLNIGNVFTSIFIAEMCLKIITADLPYHFRGNVNFDSIVALLSLADLYNT 660
QY 656 LSDNRSFLASURVLRVFKLAKSWPTNLTKIIGHSVAGALNLTAVLVIVFVFSVGM 715
Db 661 LOKRWPFLSRVLRVFKLAKSWPTNLTKIIGHSVAGALNLTAVLVIVFVFSVGM 720
QY 716 RLFGTKFNKTAVATQERPR-----RRWMDNFYHSLVVRILTCGGEWENMG 763
Db 721 QLFGRSFN-----SOKSPKLCNPTGPTVSCLRHWHMGDFHSLVVRILTCGGEWENMG 775
QY 764 CMQMDM-GSPLCIIVFVIMVIGKLVNLFIALLNLSFNEEKDGSLGEGTRKTKVQLA 822
Db 776 CMQEANASSLCVIFILITVIGKLVNLFIALLNLSFNEEKDGSLGEGTRKTKVQLA 835
QY 823 LDRFRATFSLHALQSCCKKCRKNKSPKKTETTESFAGENKSIDLP---DARPMKEYD 879
Db 836 LDRFRATFSLHALQSCCKKCRKNKSPKKTETTESFAGENKSIDLP---DARPMKEYD 894
QY 880 TDMALYTGQAGAP-----LAPLAEVDEDDVEYCGEGGALPTFSQHSAGVQAGDLP 928
Db 895 EELGILT---SVPKTLGVHDMTWLAPLAEVDEDDVEYCGEGGALPTFSQHSAGVQAGDLP 951
QY 929 ETQKLTSPDDQGVMEVSEEDLHLSIQSPRKKSDAVSMLSECSSTIDLDIFRNLOKTVS 988
Db 952 ENKKTSPQRVSQVEIDMFSEDEPHLTIQDPRKSDVTSILSECSSTIDLDIFRNLOKTVS 1010
QY 989 PKQDPRCFPKGLSCHFLCHTKDRKSPWLWNRTKTCYQIVKHSWFSFIFVILLSS 1048
Db 1011 PKQDPRCFPKGLSCHFLCHTKDRKSPWLWNRTKTCYQIVKHSWFSFIFVILLSS 1070
QY 1049 GALIPEDEVNLPSPQVEKLLRCTDNIETFIETLTKWVAFGRFYFTSACWLDLFLV 1108
Db 1071 GALIPEDEVNLPSPQVEKLLRCTDNIETFIETLTKWVAFGRFYFTSACWLDLFLV 1130
QY 1109 VYVSLSLMNLPSLKSFRTLRLRPLRALSOFEGMKVVVYALISAPAILNVLVLCLIFWL 1168

Db 1131 IVSVTTLINMELKSFRTLRALRPLRALSQEGKVVVVALIGAIPAILNVLVCLIFWL 1190
Qy 1169 VFCILGNVLFSKGRGCEINGTDINMYLDTEVPNRQCNISNYSMKVPQVNFDMVGNAYL 1228
Db 1191 VFCILGVVFFSGKFKGKINGTD--SVINYITIITNKSCQESGNFQWINKVNFDMVGNAYL 1248
Qy 1229 ALLQVATYKGLWETMNAVDSREKQDPDEANLYAYLYFVFIIFGSFFTLNLFIVGII 1288
Db 1249 ALLQVATFKGMDIYAAVDSREKQDPDEANLYAYLYFVFIIFGSFFTLNLFIVGII 1308
Qy 1289 DNFNQOKKLGQDIFMTEQOKKYNNAMKLGTKPKQPIRPLNKKQAFVLDVTSQVF 1348
Db 1309 DNFNQOKKLGQDIFMTEQOKKYNNAMKLGSKPKQPIRPLNKKCOGLFVDTQOIF 1368
Qy 1349 DVIILGLIVLNMIMMAESADQPKVKTFTDILNIAFVFIETECILKVFALRQHYFTNG 1408
Db 1369 DIIILSIILNMIMMAESYNQPKAMKSIDLHNNVFIETECILKIFALRQHYFTNG 1428
Qy 1409 WNLFDVVVLSIISTLVSRLEDS--TSFPPTLFRVRLARIGRLRLVRAARGIRTLFF 1467
Db 1429 WNLFDVVVLSIISTLVSRLEDS--TSFPPTLFRVRLARIGRLRLVRAARGIRTLFF 1488
Qy 1468 ALMMSLSPLNIGLILLFVMEIYAFGMWFSKVKKGSGIDDIENFETETGSMCLFQIT 1527
Db 1489 ALMMSLSPLNIGLILLFVMEIYAILGNWFSKVNPSGIDDIENFETETGSMCLFQIS 1548
Qy 1528 TSAGWDLNLLNPMLEAKHCNSDSSQOQOIAVYVYFVYIIISFLIVNNMYIAVILENF 1587
Db 1549 TSAGWDLNLLNPMLEAKHCNSDSSQOQOIAVYVYFVYIIISFLIVNNMYIAVILENF 1607
Qy 1588 NTATEESDPLGEDDFEIFYEWKEKFDPEASQTOYSAISDADALPEPLRVAKPNKQF 1647
Db 1608 NTATEESDPLGEDDFEIFYEWKEKFDPEATQIKYSALSADALPEPLRVAKPNKQF 1667
Qy 1648 LVMDLPMVMDRLHCDMLFAFTTRVLGDSGLDTMTMEEKMEANPKKLYEPIVTT 1707
Db 1668 LVMDLPMVMDRLHCDMLFAFTTRVLGDSGLDTMTMEEKMEANPKKLYEPIVTT 1727
Qy 1708 TKRKEEGAAVIOARVYKHKMKVVKRLKDRSS-----SSHQVFCNGDLSLSDVAKVK 1761
Db 1728 TKRKEEGAAVIOARVYKHKMKVVKRLKDRSS-----SSHQVFCNGDLSLSDVAKVK 1787
Qy 1762 VHND 1765
Db 1788 VHCD 1791

RESULT 6
Q9UHM0 ID Q9UHM0 PRELIMINARY; PRT; 1444 AA.
AC Q9UHM0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT, ALTERNATE SPLICE VARIANT
DE SCN12A-S.
GN SCN12A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20090626; PubMed=10623608;
RA Jeong S.-Y., Goto J., Hashida H., Suzuki T., Ogata K., Masuda M.,
RA Hirai M., Isahara K., Uchiyama Y., Kanazawa I.,
RT Identification of a novel human voltage-gated sodium channel alpha
RT subunit gene, SCN12A.
RL Biochem. Biophys. Res. Commun. 267:262-270(2000).
DR EMBL; AF150882; AAF24980.1;
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR001696; Na_channel.

DR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00520; Ion_trans; 3.
DR PRINTS; PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1444 AA; 165738 MW; 3B5C2922B1C7C1C CRC64;

Query Match 58.1%; Score 5329; DB 4; Length 1444;
Best Local Similarity 71.5%; Pred. No. 0;
Matches 1041; Conservative 150; Mismatches 220; Indels 44; Gaps 11;

Qy 1 MEEYYPVIFPDERNRPFTSDSLAAIKRTAIQKERRKSKDAAEQPPQDLKASR 60
Db 1 MDDRCYPVIFPDERNRPFTSDSLAAIKRTAIQKERRKSKDQGEVPPQDLKASR 60
Qy 61 KLPLKLYGDIPELPLEDLDPPYKDHKTWMLNKKRTIYFSAKRALFTLFGPFLNPLRS 120
Db 61 KLPLKLYGDIPELPLEDLDPPYKDHKTWMLNKKRTIYFSAKRALFTLFGPFLNPLRS 120
Qy 121 LMIRISVHVSFMFIICTVIINCMPMANSMER---SFDNDIPEYVFIIGYILEAVIKILA 177
Db 121 LAIRVSVHLSFMFIICTVIINCMPMANSMER---SFDNDIPEYVFIIGYILEAVIKILA 180
Qy 178 RGFIVDEPFLRDPWNWLDFTVIGTATATCPGQVNLALRTPRVFRALKAISVISGLK 237
Db 181 RGFILDEPFLRDPWNWLDFTVIGTATATCPGQVNLALRTPRVFRALKAISVISGLK 240
Qy 238 VIVGALLRSVKLVDMVMTLFCLSIFALVGQQLFMGLNOKCIKHNG--PNPASNKDC 295
Db 241 VIVGALLRSVKLVDMVMTLFCLSIFALVGQQLFMGLNOKCIKHNG--PNPASNKDC 300
Qy 296 FEKEKSDFTMCGTGLGSRPCNGSTCDKTTLPNDNNYTFDNFGWFLAMFRVMTQDS 355
Db 301 FEKKENSPEFKMGCIWGNWSACSIOYECKHTKINPDYNTNFDNFGWFLAMFRVMTQDS 360
Qy 356 WERYLQRLTSGYIFVFFVVFVPLGSLYLLNTLAVVTMAYEQNRNVAEAEKEM 415
Db 361 WEKLYQQLTSGYIFVFFVVFVPLGSLYLLNTLAVVTMAYEQNRNVAEAEKEM 420
Qy 416 FOEAQQLLRKEEALVAMGIDRSSLSLQASSPKRKFPGSKTRKSFPMRGSKTAAQS 475
Db 421 FOEAQQLLRKEEALVAMGIDRSSLSLQASSPKRKFPGSKTRKSFPMRGSKTAAQS 480
Qy 476 ASDSEDDASKNPQLLEQTKRLSQNLPLVDLFDHVDPLRQRALSASVSLTITIQSERFQ 535
Db 481 GSDSEDDASKNPQLLEQTKRLSQNLPLVDLFDHVDPLRQRALSASVSLTITIMKEQSKQ 540
Qy 536 EPCFPCKGNLASKYLVWDCSPQWLICIKVLRITMTDPTTELAITICIINIVFLAVEHNN 595
Db 541 EPCLPCKGNLASKYLVWDCSPQWLICIKVLRITMTDPTTELAITICIINIVFLAVEHNN 600
Qy 596 MDDNLKTLKIGNVFTGIFTAEMLKLTIALDPYHFRHGNVFDISIVALLSLADLYNT 655
Db 601 MEASFEXMLNIGNLVFTSIFTAEMLKLTIALDPYHFRHGNVFDISIVALLSLADLYNT 660
Qy 656 LSDNRSFLASRLVRVFLAKSNPTNLTKIIGHISVAGLGNLTVTVLTVVIFSVVGM 715
Db 661 LQKRSWPLRSFRLVRVFLAKSNPTNLTKIIGHISVAGLGNLTVTVLTVVIFSVVGM 720
Qy 716 RLFTGTFKNKATAYATQERPR-----RRHMDNFYHSFLVVFRLCGEWIENMWG 763
Db 721 QLFGRSFN-----SOKSPKLCNPTGPTVSCLRHWHMGDFWHSFLVVFRLCGEWIENMW 775
Qy 764 CMQDMD-GSPLCIIVFLIMVIGLVNLTALLNLSFSNEKDGSLGEGTRTKVOLA 822
Db 776 CMQANASSLVCVIVFILTIVIGLVNLTALLNLSFSNEKDGSLGEGTRTKVOLA 835
Qy 823 LDRFRFAFSEMLHALQSFCKKCRKNSPKKETTETESFAGENKDSILP---DARPKWYD 879
Db 836 LDRFRFAFSEMLHALQSFCKKCRKNSPKKETTETESFAGENKDSILP---DARPKWYD 894
Qy 880 TDMALYTGQAGAP-----LAPLAEEVDVVEYCEGEGALPTSQHSAGVAGDPLPP 928
Db 880 TDMALYTGQAGAP-----LAPLAEEVDVVEYCEGEGALPTSQHSAGVAGDPLPP 928

Db 895 BELGILT---SVPKTLGVRHDTWLAPLAEEEDDVEFSGEDNAQRITQPEQOAYELHQ 951
Qy 929 ETQKLTSPDDQGVEMEVESEEDLHLSIQSPKKSDAVSWLSECSTIDINDLFRNLQKTVS 988
Db 952 ENKKTSPORVOSVEIDFSEDEPHLTIQDPKPKSDVTSILSECSTIDIDQDGFGLPENYV- 1010
Qy 989 PKKQDRCPFKGLSCHFTCHTKDRKSPWLWNIRKTCYQIVKHSWFESFIIFVILLSS 1048
Db 1011 PKKQPERCLPKGFCGCCFCCSVDRKKPPWVWNLNIRKTCYQIVKHSWFESFIIFVILLSS 1070
Qy 1049 GALIFEDVNLSPRQVEKLLRCDTNIFFIFLLEMLKVAFGFRYFTSAMCWLDLIV 1108
Db 1071 GALIFEDVHLENQPKIOELLNCTDIIFTHIFLEMLKVAFGFGKYFTSAMCCLDFIIV 1130
Qy 1109 VSVLSLNLNLSKSFRLRALRPLRALSOFEGMKVWVYALISATPALNVLVCLIFWL 1168
Db 1131 IVSVTLNLNLSKSFRLRALRPLRALSOFEGMKVWVYALISATPALNVLVCLIFWL 1190
Qy 1169 VFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRSCQINISYMKVPQVNFNDVGNAYL 1228
Db 1191 VFCILGVYFSGKFGKINGTD--SVINYTIITNKSQCESGNFSWINGKVFNDVGNAYL 1248
Qy 1229 ALLQVATYKGMLEIMNAADVREKDEPDPEANLYAYLVYFVFIIFGFFFTLNFIGVII 1288
Db 1249 ALLQVATEKGWMDIITAAVDSTERKEQQPEFESNSLGYIFVYFVFIIFGFFFTLNFIGVII 1308
Qy 1289 DNFNOOKKLGODIFMTTEOKKYNNAMKLGTKPKQPIRPLNKCQAFVFDLVTQV 1348
Db 1309 DNFNOOKKLGODIFMTTEOKKYNNAMKLGSKPKQPIRPLNKCQGLFVDIVTSOIF 1368
Qy 1349 DVITLGLVLNMIIMAESADQDKVKTFDLNTAFVVIETIECLIKVAFALRQHYFTNG 1408
Db 1369 DIIITSLILNLSWMAESYNQPKAMKSILDLHNNVVFVITIECLIKIFALRQHYFTNG 1428
Qy 1409 WNLEDCVVVLSIIS 1423
Db 1429 WNLEDCVVVLSIIS 1443

RESULT 7
Q9JJV9 PRELIMINARY; PRT; 2019 AA.
ID Q9JJV9 AC Q9JJV9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE VOLTAGE-GATED SODIUM CHANNEL.
GN SCN5A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=HEART;
RA Zimmer T., Beendorf K.;
RT "the mouse heart sodium channel (mhl): cloning and characterization of
RT alternatively spliced variants.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271477; CAB70096.1; -.
DR MGD; MGI:98251; Scn5a.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR002111; Cat_channel_Trbp.
DR InterPro; IPR001682; Cat_channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; ion.trans. 4.
DR SMART; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
KW Ionic channel.
SQ SEQUENCE 2019 AA; 227620 MW; FDB48750D599B89A CRC64;

Query Match 51.6%; Score 4730; DB 11; Length 2019;
Best Local Similarity 50.1%; Pred. No. 0;
Matches 976; Conservative 286; Mismatches 423; Indels 262; Gaps 32;

Qy 15 NFRPFTSLAAIKKRIAIQKER-----KSKDKAAAEPPQPPQLDQKASRKLPLKLYGDI 69
Db 12 SFRRTRESLAARMAEKQARGSATQSESEGLPEEAPRPDLQASKKLPOLYGNP 71
Qy 70 PPELVTKPLEDLDPPYKDKHTFMVNLNKRRTYRFSAKRALFGLFPNPLRSLRIMIRISVH 129
Db 72 PRELIGEDLDPPYSTOKTFIVLNKGTIFRSATNALYVLSFHPVRRAAVILVHS 131
Qy 130 VFSFELICTVIINCMFMANSMERSFDNDIP-----EYVFIGIYILEAVIKILARGFIVD 183
Db 132 LFSMLIMICTIITNCVFMA-----QHDPPTWTKVYETFTYATYTFESLVKILARGFCLH 184
Qy 184 EFSFLRDPNNWLDFTVIGTAIATCPGSGVNLSSALRTRFRVFRALKAISVISGLKIVGAL 243
Db 185 AFTFLRDPNNWLDFTSVIVWAYTEFV-DLGNVSALRTRFRVLRALKTIVISGLKIVGAL 243
Qy 244 LRSVKVLVDVWVLTFLCLISIFALVGOQLFMGLILNOKCIKHNC---GNPASHKD----- 294
Db 244 IQSVKKLADVWVLTVFCLSVFALIGLQFMGNLRHKVNRFTELNGTNGSVEADGIVNNS 303
Qy 295 -----CPEKEKDSDFIMCGTWLGSRPCNGSTCDKTTLPNDNNYTKFDNFGWFL 345
Db 304 LDVYNDPANVLLKNGTTDVLICGNSDAGTCPEGYRCLKAGENPDHGTSEDSAWAFL 363
Qy 346 AMFRVMTQDSWERLYRQILRTSGIYFVFFVVFVIFGLSYFLINLTAVVTVAYEYEQNRNV 405
Db 364 ALFRMTQDWERLYRQILRSAGKIYMFVFLVFLGFLVNLVILAVVAYEYEQNAT 423
Qy 406 AAETAEKMFQEAQOLLREEKEALVANGIDRSSNLNSIQASFSF-----KKRKFFG 457
Db 424 IAETEEKEKTFQEAEMELKKEHEALTIRGVDTVSRSSLEMSPLAPVTNHERSKRKRLLS 483
Qy 458 SKT-----RKSFFMRGSKTA-----QASASDS 479
Db 484 SGTEDEGDDRLPKSDSEDPALNOLSLTHGLSRTSMPRSRSGSIFTFRRRDQGEADF 543
Qy 480 EDDASK----- 485
Db 544 ADDENSTAGESHRTSLVWPWPLRRPSTQGPFGTAPGHVNLGNKRNSTVDCNVVSL 603
Qy 486 -----NPOLLEQ-----TKRLSNLP-VDLFDHVDPLHRQ 515
Db 604 LGAGDAEATSPGSHLLRPVLDLPPDTTTPSEPGGPQMLTPQAPCAGDFEE---PGARQ 660
Qy 516 RALSAVSLTITIQOEKFPQPCPGKNLASKYLWDCSPOWLCKIKKVLRTIMTDPTE 575
Db 661 RALSAVSLTSALEESHRKCPPCWNRFAQHYLIWECCLPMWSIKQKVFVMDPFAD 720
Qy 576 LAITICIINTVFLAVEHNNDDNLTKITLIGNWWVFTGIFTAEMCLKIADLPYHFRHG 635
Db 721 LTITWCIVNLTFMALEHYNNMTAEFEMLQVGNLVFTGIFTAEMFKIADLPYIFQOG 780
Qy 636 WNVFDSIVALLSLADVLNTLSDNNRSLASLRVLRVFKLAKSWPTLNTLKIIGHSVGA 695
Db 781 WNVFDSIVALLSMLGLSRM--GNLSVLSFRLLRVFKLAKSWPTLNTLKIIGNSVGA 838
Qy 696 LGNLTVLTIVVFPFVVGMLRFGTKFNKATAYATQER---PRRRVHMDFYHSLFVFPRI 752
Db 839 LGNLTVLTIAIIVFVAVVGMOLFKNYSRLRHRISDSGLLP--RHHWMDFFHAFILFRI 896
Qy 753 LCGEWIENWGMQMDGSPICIIIVFLIMVIGKLVNLNLTALLNLSFSNE-----BKD 807
Db 897 LCGEWIETWDCM--EVSQSCLLVFLVLLVWVIGNLVNLNLTALLLSFSFADNLTPADEP 955
Qy 808 GSLEGETRKTQVQLADRFRAFSPFMLHALQSFCCCKCRK----- 848
Db 956 GEM-----NNLQALARIQGLRFVKKRTTWDVFCGGLLRRRRPPKPAALATHSQLPSCITT 1009

Db 532 SHRGLLLGGAGGQOGLPRSPLOPSPNDPSRHGDEHQPPP-----TSELAPGADVSA 586
Qy 505 FD-----EHDV-DLPHRORALSAYSILITITIQEOEKFOEPCPCGKNLASKYLYWD 553
Db 587 FDAGOKKTFLSNEYDEDFRAQRAMSVSIISVLEESQKPPCLTSLSQKYLWD 646
Qy 534 CSPOWLCKIKVLRTIMTDPFTELATITICIIINTVFLAVEHHNMDNLTKILKIGNVFTG 613
Db 647 CCPMVKLTILFGLVTDPAELTITLCIVVNTIFMAHEHGMSPTEAMLOIGNIVTI 706
Qy 614 IFIAEMCLKIITALDYPHYFRGHWVFDISVALLSLADVLNLTSLNNRSFSLASLVRVF 673
Db 707 FFTAEMVFKIIAFDPYFYFQKWNFDICIIIVTSLEL--GVAKGKLSVLSKRSFRLRVF 764
Qy 674 KLAWSPTLNTLIKTIHGSVAGLNLTVLTIIVFISVGMRLFGTKF--NKTAYATOE 731
Db 765 KLAWSPTLNTLIKTIHGSVAGLNLTIILAIIVFVALGKQLLGENYRNRKNISAPH 824
Qy 732 RPRRHHMDFHSLVFRILCGEWIENMGCMODGSPLCIIVFVLINWIGKLVVLN 791
Db 825 EDWPRHMHDFHSLVFRILCGEWIENMACM--EVGKSCICILFLTVVWGLNVLN 883
Qy 792 LFIALLLNSFNE-----EKDGLSEGETRKTQVQALDRFRRAFSFMLHALQSFCCKR 846
Db 884 LFIALLLNSFADNLTAPEDDGEV-----NNLQVALARIOVFGHRTKOALCSFPRS- 936
Qy 847 RKNSPKPKETTE-----SFAGEN-----KDSILPDARPKWEYDMDALYTQ 888
Db 937 --PPQPKAEPVLVVKLPLSSKAENHIAANTARGSSGLOAPRDRHSDFIANPTVW 994
Qy 889 AGAPLA-----PLAEVEDD-----VEYCGEGGALPTSQHSAGV 921
Db 995 VSVPLAEGESDLDDLEDGGEQAQSQFQEVIPKGOEQLOQVERCD--HLTPRSPGT 1052
Qy 922 QAGDLPETKOLTSPDDQGVMEVSEEDLHLISQSPRKKSDAVSMLSECTIDLND--- 978
Db 1053 SSEDLAPSLG-----ETWKDESVP--QAPAEVDDTSS--SEGSTVDCLDPEE 1096
Qy 979 IFRNLQTVSPKQPDRCFPKGLSCHFLCHTKDRKSPWLWNWNRKTCYQIVKISWFES 1038
Db 1097 ILRKLPELADLEEDDCFTGCIHPCCKLDTTKSPWDVQGWQVRYKTCYRIVERHWPES 1156
Qy 1039 FTIFVILLSSGALFEDVNLSPPOVEKLLRCTDNIFTFILLEMILKWAFGPRRYFTS 1098
Db 1157 FTIFMILLSSGLAFEDYILOKPTVKALLEYTRVFFIFVFEMLLKWAVGFKKYFTN 1216
Qy 1099 AWCWDLFIVVSVLSL-----MNLPSLSKSFRTLRALRPLRALSQFEGMKVYVALIS 1151
Db 1217 AWCWDLFIVVSVLSL-----MNLPSLSKSFRTLRALRPLRALSQFEGMKVYVALIS 1151
Qy 1152 AIPALNLVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINWYLDFTVP-----NRSQC 1206
Db 1277 AIPSLMNVLLVCLIFWLVFISGVNLFAGKFWRCINYTD-----GEFSLVPLSVNNKSDC 1332
Qy 1207 NISN-----YSWKVPOVNDVGNVALLQVATYKGLWEIMNAVDSREKDEQDFEANL 1262
Db 1333 KIONSTGFFWVNVKVNFDNVAMGYLALLQVATFKGWMDIIVAAVDSREVNMQKWDNV 1392
Qy 1263 YAYLVVVFIIFGSFTLNLFIIGVIIDNFNOQKKLGGODIFMTBEQKKYNNAMKLGTK 1322
Db 1393 YWYLVFVFIIFGGFTLNLVGVIIIDNFNOQKKLGGODIFMTBEQKKYNNAMKLGSK 1452
Qy 1323 KPQKPIRPLNKCQAFVLDVTSQVFDVILGLIVLNMIMWASADQPKDKVKTFDILN 1382
Db 1453 KPQKPIRPLNKCQAFVLDVTSQVFDVILGLIVLNMIMWASADQPKDKVKTFDILN 1382
Qy 1383 IAFVVFIECLIKFALRQHYFTNGWNLFCVGVVLSIISTVLSR--LEDSISFPPTLF 1441
Db 1513 QFFVAVFTGECVMKMFALRQHYFTNGWNVDFIVVLSIASLISAILKLSQSFSPFLF 1572
Qy 1442 RVRLARIGRLRLVRAARGIRTLFLFALMSLPSLNFNTGLLFLVMFYTAIFGMSWFSKV 1501
Db 1573 RVRLARIGRLRLVRAARGIRTLFLFALMSLPSLNFNTGLLFLVMFYTAIFGMSWFSKV 1501

Qy 1502 KKGSGIDDIFNETFTGSMCLCFQITTSAGWDTLLNMLE-AKEHC-----NSSQSDSC 1554
Db 1633 RWEAGIDMWFNFOITFANSMCLCFQITTSAGWDTLLNMLE-AKEHC-----NSSQSDSC 1692
Qy 1555 QOQOIAVYVYSYIIISFLIVVMYIAVILENFATSEESDPLGDDFEIFEYVWEKFD 1614
Db 1693 GSPAGVGIIFTYIIISFLIVVMYIAVILENFATSEESDPLGDDFEIFEYVWEKFD 1752
Qy 1615 PEASOFIOYSALSDFADALPEPLRVAKPNKFQFLVMDLPMWMDRLHMDVLFATFTRVL 1674
Db 1753 PEATOFITFSALSDFADTLGSLRIPKPNRNLIQMDLPLVPGDKIHCLDILFAFTKNVL 1812
Qy 1675 GDSSGLDMMKTMEEKFMEANPFKLYLPVITVTTTKKEEEOGAAVLOQAYRKHM 1728
Db 1813 GESGELDSLKANNEEKFMATNLSKSYEPFIATTLRWKQEDISATVIQKAYSIV 1866
RESULT 9
P70276 PRELIMINARY; PRT: 1958 AA.
ID P70276
AC P70276:
DT 01-FEB-1997 (TREMBlrel. 02, Created)
ET 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
PT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
IE SODIUM CHANNEL, TYPE X, ALPHA POLYPEPTIDE (VOLTAGE-GATED SODIUM CHANNEL).
DE CHANNEL.
GN SCN10A OR SNS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
KW [1]
RP SEQUENCE FROM N.A.
FC STRAIN=129/SV;
ZX MEDLINE=97288517; PubMed=9143495;
XA Souslova V., Fox M., Wood J.N., Akopian A.N.;
RT "Cloning and characterization of a mouse sensory neuron tetrodotoxin-
resistant voltage-gated sodium channel gene, Scn10a";
KL Genomics 41:201-209(1997).
DR EMBL; Y09108; CAA70325.1; -;
DR MGD; MGI:108029; Scn10a.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR000048; IQ.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans. 4.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
KW Ionic channel.
KW SMART; SM00015; IQ; 1.
SQ SEQUENCE 1958 AA; 220402 MW; AE3811C17721EB72 CRC64;

Query Match 49.7%; Score 4555; DB 11; Length 1958;
Best Local Similarity 50.4%; Pred. No. 0;
Matches 956; Conservative 273; Mismatches 444; Indels 224; Gaps 34;

Qy 15 NFRPFTSDSLAAIKKRIATQKERRKSKDKAAAE----PQPRQLDKASRKLPLKYGDIP 70
Db 12 NFRFTPSLAFIEKQIAAHRAAKKGRTKQKQKDKSEKPRQLDKACNLPRFYGELP 71
Qy 71 PELVTKPLEDDLPYYKDHKTVMFNKKRTIYRFSKRALFILGPNPNRLSRMIRSVHSV 130
Db 72 AELVGEPLDLPYYSTHRTFTILLNKSRTISRFSATWALWLFSPENLIRRTAIVKSVHSW 131
Qy 131 FSMFTICTVITNCHEMANSMBERSFNDIP--EYFVIGIYILEAVIKILARGFIVDESF 187
Db 132 FSIFITVILVNCVCMTRT-----DLPEKLEYVTVVYTFEALIKILARGFIVDESF 184
Qy 188 LRDPNNWLDVIGTGTATCFPGSQVNL---SALRTRFRVFRALKAISVISGLKVIIVGALL 244
Db 185 LRDPNNWLDVSVITLA-----YVGAADVLRIGSLGTRFRVLRALKTVSVIPGLKVIIVGALI 240

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QY 245 RSVKLVDMVMTLFCLSIFALVQQLFMGTLNOKCIKHNCGNPASN-----KDCFEK 298
D 241 HSVKRLADVTLTVFCLSVFALVQLFKGNLKNKIKNGTDHPKADNLSSEMAEDFIK 300
QY 299 EKUSEDIMCGTWLGRPCPNCGSTCDKTTLPNDNNYTKFNFNGSWFLAMPFVMTQDSWR 358
D 301 -PGTDPDLGCGSDAGCHPCNGYVQKTPDNPENYTSFDSFAWFLSLFRLMTQDSWR 359
QY 359 LYRQILRTSGYVFFRVVFLGSLFYLLNLTLAVTMAVEEQNRNVAATEAKEKFOE 418
D 360 LYQOTLRASGMVAVFVFLGSLFYLLNLTLAVTMAVEEQNRNVAATEAKEKFOE 419
QY 419 AQQLREKEALVAMGIDRSSL-----NSLQAS 446
D 420 ALEVLQKEQVLAALGIDTTSFYSHSGSPLASKNANRRPRVKSRVSEGGTDDNRSQSD 479
QY 447 SFSPPKKRFTG-----SKTRKSFMRG 468
D 480 PYNORRMSFTLSSGRRRRASHGVSFHFRAFPDSQVSPDPDGLDGVFGHQDESRENILG 539
QY 469 SKTAQAS-ASDSEDDASKNP-----OLLEOTKRLSONLP-----VDLFDDEH----- 508
D 540 RGACQAGPLRSPQLPQSPNCRKHGKQGLMPTGELAAAGTPEGPALDAAQGNFLSAGY 599
QY 509 -VDPHLRQALSAVSILITITIQEQKQEPFCPCGNLASKYLWDCSPQWLCIKKYLRT 567
D 600 LNEPRAORAMSVSVIMTSVIEELEESKLCPCCLISFAQKYLWECCKPKWKFKVLE 659
QY 568 IMTDPFTLAIITCIINTVFLAVEHNNMDNLKTLKIGNVPTGTFIAEMLKLIITLD 627
D 660 LVTDPPFAELTITLCIVVNTVFMAMEHYPMTDADFAMQAGNIVTFTFTEMAFKIATD 719
QY 628 PYHFRGNVNFDSIVALLSLADLYNTLSDNNRSEFASLRVLRFVFLAKSWPTNLTK 687
D 720 PYYFQKKNIFDCVIVTVSLEL--SASKKGSLSVLSRLRLRVFLAKSWPTNLMLIK 777
QY 688 IIGSVGALGNLTVLTVIVFISVGMRLFGTKF--NKTAYATQERPRRRHMDNPNYS 745
D 778 IIGSVGALGNLTFLAIIVFIFALVQKLLSENCGRRDGVSVWNGEKLRRWHMCDFFHS 837
QY 746 FLVYFRILCGEWIENMGCCQMDGSLPLCIIVFLVIMVIGLVLNLFIALLLNSFSNE- 804
D 838 FLVYFRILCGEWIENMVCM-EVSONYICLTLFVLVGLNVLNLFIALLLNSFSADN 896
QY 805 ----EKDGSLEGETRKVKOLALDRFRRAFSEMLHALQSCCKCRK----- 848
D 897 LTAPEDDGEV-----NNLQALARIQVLGHASRAITSYRSHCRFRWPKVETQLGMKP 950
QY 849 -----NSPKPKETTESFAG--ENKDSILPDARPWKEYDMDALYTQAG 890
D 951 PLTSCKVENHIATDAVNAAVGNLTKPALSGPKENHGDFTIDPNVW-----VS 997
QY 891 APLA-----PLAEVEDDVEYC-----GEGGALPTSQHSAGVQAGDLPPETKOLTS 935
D 998 VPIAEGESDLEDEEDVEQASQSSWQBPESKQOQLLPQVKCNHQHAARSP--TSGMS 1055
QY 936 PDDQGVEMEVFSEDLHLSTQSPKKSADVMSMLSECTSIDLND--IFRNLQKTVSPKKQ 992
D 1056 EDLAPYLGERWKRD--NPOVPAEGVDDTSS-SEGSTVDCPDPEELIRKIPELAELDE 1111
QY 993 PDRCFPPKGLCHFKLTKDRKSPWLWNNIRKTCYQIVKHSWFESFIIFVILLSSGALI 1052
D 1112 PDDCFTEGCTRRCPCKVNTSKSPWATGWQVRYKTVIHEHSWFESFIIFMILLSSGTLA 1171
QY 1053 FEDVNLRSRQVEKLLKCTONIFTFELLEMILKWAFAFRYRITSACWLDLFLVVSV 1112
D 1172 FEDNYLEKPRKSVLSEYTDVFTFIFVFEMLLKWVAYGKKYFTNACWLDLFLVNLIS 1231
QY 1113 LSLM-----NLPSLKSFTRLRALRPLALSOFEGKVVVYALISAIPATLNVLLVCLI 1165
D 1232 TSLIAKILEYSDVASIKALRTLRLRALRPLALSREFGRVVVDVLAIGVAPISIMNVLLVCLI 1291
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RESULT 10

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Q62968 PRELIMINARY; PRT: 1956 AA.
AC Q62968;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE SODIUM CHANNEL PN3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=8663093;
RA Sangameswaran L.B., Delgado S.G., Fish L.M., Koch B.D., Jakeman L.B.,
Stewart G.R., Spe P., Hunter J.C., Eglen R.M., Herman R.C.;
EL J. Biol. Chem. 271:13292-13292(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198040; PubMed=8626372;
RA Sangameswaran L., Delgado S.G., Fish L.M., Koch B.D., Jakeman L.B.,
Stewart G.R., Spe P., Hunter J.C., Eglen R.M., Herman R.C.;
PT "Structure and function of a novel voltage-gated, tetrodotoxin-
resistant sodium channel specific to sensory neurons."
RL J. Biol. Chem. 271:5953-5957(1996).
DR EMBL; U53833; AAC52619.1; -.
DR InterPro; IPR000636; Catlon_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR001696; Na_channel.
LR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00533; ion_trans; 4.
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Db 1650 FCMNSFAYVYKBDGINDMFNFETFGNSMCLFQITTSAGDGLLAPILNSKPPDCDPKKV 1709
QY 1545 HCNSSQSDCOQJAVYFVSYIIISFLVVMYIAVILENFNTATESEDPLEDDEFE 1604
Db 1710 HPGSSVEGCGNPSVGIFFVSYIIISFLVVMYIAVILENFNTATESEDPLEDDEFE 1769
QY 1605 IFYEWKFDPRASQIYQYVYFVSYIIISFLVVMYIAVILENFNTATESEDPLEDDEFE 1664
Db 1770 MEYEWKFDPRASQIYQYVYFVSYIIISFLVVMYIAVILENFNTATESEDPLEDDEFE 1829
QY 1665 VLFATTRVGLDSSGLDNTKMTWMEKFEANPDKLYEPIVTTTKRKEEEOGAAYQRAY 1724
Db 1830 ILFAFTKRVLGSEMGDSLSRQMEERFMSANPSKVSYPEITTLTKRKQEDVSATVIQRAY 1889
QY 1725 RKHMEKMKVLRKDRSSSS 1743
Db 1890 RRY-----RLRONVARNISS 1903

RESULT 12
Q63554 PRELIMINARY; PRT: 1957 AA.
AC Q63554;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE VOLATAGE-GATED SODIUM CHANNEL.
GN SNS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DRG;
RX MEDLINE=96138382; PubMed=8538791;
RA Akopian A.N., Sivillotti L., Wood J.N.;
RT "A tetrodotoxin-resistant voltage-gated sodium channel expressed by
sensory neurons";
RL Nature 379:257-262(1995).
DR EMBL; X92184; CAA63095.1; -
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR002111; Cat_channel_TripL.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1957 AA; 219913 MW; 7527164171F3A978 CRC64;

Query Match 49.6%; Score 4545.5; DB 11; Length 1957;
Best Local Similarity 51.0%; Pred. No. 0;
Matches 966; Conservative 265; Mismatches 446; Indels 217; Gaps 36;
QY 15 NRPFTSDSLAAIKKRIAIQIKERKSKDKAAAE-----PPRPOLDKASRLPKLYGDIP 70
Db 12 NFRFTPSLAEIEKQIAHAARAKARTKHGQEDKGEKPRQLDKCNQLPKFYGEIP 71
QY 71 PELVTKPLEDDPPYKDHKTVMVNLKRTIYFRSAKRALFTLGPFPNPLRLMIRISVHSV 130
Db 72 AELVGEPLDPPYKDHKTVMVNLKRTIYFRSAKRALFTLGPFPNPLRLMIRISVHSV 131
QY 131 FSMFICIVILNCMFMANSERSFNDIP---EYFVIGIYILEAVIKILARGFIVDEFSF 187
Db 132 FSFIITILVNCVCMTRT-----DLPERVEYFTYITFALIKILARGFIVDEFSF 184
QY 188 LRDPMNLDFIVIGTAITCFPGSOVNL---SALRTFVRALKALISVIGLKVIIVGALL 244
Db 185 LRDPMNLDFIVIGTAITCFPGSOVNL---SALRTFVRALKALISVIGLKVIIVGALL 240
QY 245 RSVKLVDMVVLTLFCLSFIFALVGQOLPMGILNOKCIKHNCGPNPASKNCKCFEKE----- 299
Db 245 RSVKLVDMVVLTLFCLSFIFALVGQOLPMGILNOKCIKHNCGPNPASKNCKCFEKE----- 299

Db 241 HSVKRLADVTILTVFCLSVFALVGLQKFKGNLKNKNCIRNGTDPHKADNLSSMAEYIFTK 300
QY 300 KDEDFIMCGTWLGRPCPNPGSTCDKTTLPDNNVTKDFNFWSEFLAMPVMTQDSWERL 359
Db 301 PGTTPPLCGNSDAGHCPGGYVCLKTPDNPONTSETDSFAWFLSLFRLMTQDSWERL 360
QY 360 YROIURTSGLYVFFVVFVIFGLSYFLNLLTLAVVTMAYEONRNVAATEAKEMFOEA 419
Db 361 YQOTLRASGKMYVFFVIFGLSYFLNLLTLAVVTMAYEONRNVAATEAKEMFOEA 420
QY 420 QOLLREEKALVAMGIDRSSLSLQASSFSF-----KKRKFEGS----- 458
Db 421 LEVLQKEQLEALGIDTTSLSHSGSPLASKNANERRPRVKSRVSEGSTDDNRSPQSDP 480
QY 459 --KTRKSFMRGSKTAQASD-----SEDDA----- 483
Db 481 YNQRMSFLGLSSGRRRASHGVSFHRAPSQDISFPDGTIPDDGVFHGDOESRRGSILLG 540
QY 484 -----SKNP-----QLLEQTKRLSQNL-----VDL 504
Db 541 RGAGOTGPLPRSPPLQSPNPGRRHGEEOGLVPTGELTAGEPGALHTTGOKSFLSAGY 600
QY 505 FDEHVDPLHRQALSAVSILITITIOEQEFQPCPCGKNLASKYLWDCSPQWLICIRKV 564
Db 601 LNE---PFAQRAMSVSVSMTSVIEELESKLKCPCLISFAQKYLWDCSPQWLICIRKV 657
QY 565 LRTIMTDFTELATITCIINTVFLAVEHHNMDNLKTLIKGNVWVFGIFIAEMCLKIT 624
Db 658 LFLVTDTPFAELTITLCIVWTVFMAMHYPMTDADMLQAGNIVTVFFTEMFAFKII 717
QY 625 ALDPVHYFRHGWNVFDSIVALLSADLVNLTSLDNRRSFLASLRLVFLKLSAKSPTLNT 684
Db 718 AFDPIYFQKKWNIFDCVITVTSLEL--SASKGSLSVLRLLRLVFLKLSAKSPTLNT 775
QY 685 LIKIIGHSVAGLNLTVTLTVVIFSVVGMRLFTGKF--NKTAYATOERPRRRHMDNF 742
Db 776 LIKIIGSVAGLNLTVTLTVVIFSVVGMRLFTGKF--NKTAYATOERPRRRHMDNF 835
QY 743 YHSFLVFRILCGEWIENMWGQMDGSPICIIIVFLIMVIGLWLVNLFALLINSFS 802
Db 836 FHSFLVFRILCGEWIENMWGQMDGSPICIIIVFLIMVIGLWLVNLFALLINSFS 894
QY 803 NE-----EKGSLGETRKTQVOLDLDRFRAFSPMLHALQSCFCKCK-----RNS 850
Db 895 ADNLTAPEDDGEV-----NNLQALALRIQVLGHRASRAIASYISSHCRFHPKPVETQLG 948
QY 851 PKPFTTESFAGENKDSILPDA-----RP-----WKEYDTDMALYTGQAGAPL 893
Db 949 MKPPLT-----SSEAKNHIAATDAVSAAGNLTKPALSSPKENHGDEFTDPNVW---VSVPI 1001
QY 894 A-----PLAEVEDDVEYC-----GEGGALPTSQHSAGVQAGDLPETKQLTSPDD 938
Db 1002 AEGSDLLDELEDMEQASQSSWQEDPRGQEQQLPOVKCNHQAAARS--ASMMSSDL 1059
QY 939 QGVMEVSEEDLHLSIQSPKKSDAVSMSECTIDLND---IFRNQKTVSPKQKQPR 995
Db 1060 APYLGESWKRKD---SPOVPAEGVDDTS--SEGSIIVCDPDEILIRKIPELADDDLEPDD 1115
QY 996 CFPKGLSCHFLCHKTRKSPVLMWNIKTCYQIVKHSWFESFIFVILLSSGALIFED 1055
Db 1116 CFTEGCTRRCPCCNVNTSKSPWATQWVKTCYRIVEHSWFESFIFVILLSSGALIFED 1175
QY 1056 VNLPSRPOVEKLLRCTDNIFTIFLLEMLKWAAGCFRRYFITSACWCLDFLIVVSVLSL 1115
Db 1176 NYLEEKPRVKSLEYETDRVFTFIFVEMLLKWAAGCFRRYFITSACWCLDFLIVVSVLSL 1235
QY 1116 M-----NLPSKSFRTLRALRALSOPGKMWVVALISAIPATLVLLVCLIPWL 1168
Db 1236 IAKILEYSDVASIKALRTRLRALRSRFGMRVMDALVGAIPMNVLLVCLIPWL 1295
QY 1169 VFCILGVNLSFGKFGRCINGTDINMY--LDTEFVNRSCQNTISN---YSWKVPQVNFON 1222
Db 1296 IFSIMGVNLFAKFSKCVD--TRNNPFSNVNSTMVNKNSECHNQNSTGHFFFWNVKVFND 1354

QY 190 DPWNLDFTVIGTATATCPGQSVNLSALRTRFRVFRALKATISVIGLKVIVGALLRSVKK 249
Db 186 DPWNLDFTVIVFAYLITEV- NLGNVSALRTRFRVLRALKTISVIPCLKTIIVGKALIQSVK 244
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Search completed: February 27, 2002, 01:38:16
Job time: 360 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 22:39:07 ; Search time 8647.11 Seconds
(without alignments)
570.440 Million cell updates/sec

Title: US-09-646-224A-3

Perfect score: 299

Sequence: 1 atctaggcagcgtgtttt.....cgacaatctcggaggcttt 299

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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20: em_or:*

21: em_ov:*

22: em_pat:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	276.4	92.4	5728	9	AF150882	Homo sapi
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4	204.4	68.4	6237	9	AF188679	Homo sapi
5	167.8	56.1	5908	6	E36122	Nucleic aci
6	160.4	53.6	5334	6	E36125	Nucleic aci
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10	158.4	53.0	5897	6	AX017217	Sequence
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13	44.2	14.8	6726	4	CFU60590	Canis fami
14	38.6	12.9	128398	9	AC004817	Homo sapi
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16	38.4	12.8	7052	6	A58857	Sequence 5
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25	36	12.0	145105	2	AC018432	Homo sapi
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ALIGNMENTS

RESULT 1

AX017219

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

human.

Sequence 3 from Patent WO9947670.

AX017219.1 GI:10042139

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;

1 (bases 1 to 299)

Tate,S.N., Grose,D.T. and Hick,C.A.

Mammalian sodium channel proteins

Patent: WO 9947670-A 3 23-SEP-1999;

TATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS

(GB); HICK CAROLINE ANNE (GB)

Location/Qualifiers

1..299

/organism="Homo sapiens"

PAT 07-SEP-2000

Kanazawa, I.
Direct Submission
Submitted (27-NOV-1998) Neurology, Graduate School of Medicine,
Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Location/Qualifiers
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BASE COUNT 1842 a 1446 c 1410 g 1830 t

Query Match
Best Local Similarity 92.4%; Score 276.4; DB 9; Length 6528;
Matches 291; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db 360 TTGACCTAAAGGCTCCAGGAAGTTGCCAGCTCTATGGCAGCATTCCTCTGAGCT 417
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RESULT 4
AF188679
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DEFINITION Homo sapiens voltage-gated sodium channel type XI alpha subunit
(SCN11A) mRNA, complete cds.
ACCESSION AF188679
VERSION AF188679.1 GI:6572949
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6237)
Dib-Hajj, S.D., Tyrrell, L., Cummins, T.R., Black, J.A., Wood, P.M. and
Waxman, S.G.
Two tetrodotoxin-resistant sodium channels in human dorsal root
ganglion neurons
FEBS Lett. 462 (1-2), 117-120 (1999)
20047838
2 (bases 1 to 6237)
Dib-Hajj, S.D., Tyrrell, L., Cummins, T.R., Black, J.A. and Waxman, S.G.
Direct Submission
Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,
Bldg. 34, 950 Campbell Ave., West Haven, CT 06516, USA
Location/Qualifiers
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E36122
LOCUS E36122 5908 bp DNA PAT 07-FEB-2001
DEFINITION Nucleic acid encoding sodium channel of nerve tissue.
ACCESSION E36122
VERSION E36122.1 GI:13022505
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 5908)
AUTHORS Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.
TITLE Nucleic acid encoding sodium channel of nerve tissue
JOURNAL Patent: JP 1999235186-A 1 31-AUG-1999;
F HOFFMANN LA ROCHE AG
COMMENT OS Rattus sp. (rat)
PN JP 1999235186-A/1
PD 31-AUG-1999
PF 20-NOV-1998 JP 1998331769
PR 20-NOV-1997 US 60/066225
PI PAUL SHATUA DAITORICHI, LINDA MARIE FISH, RINA KEIRU, PI
DOUGLAS KENESU RAMBERT,
LAKSMI SANGEIMUSUWARAN
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12N15/02, C12P21/02, PC
C12P21/08,
C12P21/08,
PC C12Q1/68, G01N33/53, G01N33/57, G01N33/68//((C12N5/10, C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/08, C12R1:91), C12N15/00, C12N5/00,
PC C12N15/00,

QY 53 gtgctgtctctgtcctgaggtgaagatgacagatgctaccagtaatttcctc 112
Db 51 GTGTCTTCTGCCCTCCTCAGGGTGAAGATGGAGAGAGGACTACCCGGTGATCTTCCC 110
QY 113 agatgagcggaatttcgcccccttcacttcctcctgctgctgcaattgagaagcgat 172
Db 111 GGACGAGCGGAATTTCCGCCCTTCCACTTCCGACTCTCTGGCTGCCATAGAGAGCGGAT 170
QY 173 tgccatccaaagagagaaaagatctaaagaccagacagagagaagtaacccagcctca 232
Db 171 TGCTATCCAAAGAGAGAGAGAGTCAAGAGCAAGCGGCGGAGTGCAGCCCGAGCTCG 230
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ORIGIN

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Best Local Similarity 82.6%; Pred. No. 9.7e-41;
Matches 204; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
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QY 113 agatgagcggaatttcgcccccttcacttcctcctgctgctgcaattgagaagcgat 172
Db 111 GGACGAGCGGAATTTCCGCCCTTCCACTTCCGACTCTCTGGCTGCCATAGAGAGCGGAT 170
QY 173 tgccatccaaagagagaaaagatctaaagaccagacagagagaagtaacccagcctca 232
Db 171 TGCTATCCAAAGAGAGAGAGTCAAGAGCAAGCGGCGGAGTGCAGCCCGAGCTCG 230
QY 233 acctcagcttgacctaagggcctccaggaagtggccaa-cctctatggcgacaatcctcg 291
Db 231 GCCTCAGCTTGACCTTAAGGCCCTCCAGGAAGTTACTRAGCTTTATGGTGACATTCGCC 290
QY 292 gaggctt 298
Db 291 TGAGCTT 297

RESULT 6
E36125
LOCUS E36125 5334 bp DNA PAT 07-FEB-2001
DEFINITION Nucleic acid encoding sodium channel of nerve tissue.
ACCESSION E36125
VERSION E36125.1 GI:13022508
KEYWORDS JP 1999235186-A/4.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 5334)
AUTHORS Paul,S.D.L.L., Fish,R.K.D.D., Rambert and Laksmi,S.
TITLE Nucleic acid encoding sodium channel of nerve tissue
JOURNAL Patent: JP 1999235186-A 4 31-AUG-1999;
F HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 1999235186-A/4
PD 31-AUG-1999
PF 20-NOV-1998 JP 1998331769
PR 20-NOV-1997 US 60/066225
PI PAUL SHATUA DAITORICHI, LINDA MARIE FISH, RINA KEIRU, PI
DOUGLAS KENESU RAMBERT,
LAKSMI SANGEIMUSUWARAN
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12N15/02, C12P21/02, PC
C12P21/08,
C12P21/08,
PC C12Q1/68, G01N33/53, G01N33/57, G01N33/68//((C12N5/10, C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/08, C12R1:91), C12N15/00, C12N5/00,
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Best Local Similarity 83.99; Pred. No. 1.8e-38;
Matches 193; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

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Qy 130 gcccttcactccagactctctgctgcaattgagaagcgattgccatccaaaggaga 189
Dy 73 GCCCTTCCACTTCGACTCTCTGGCTGCCATAGAGAAGCGGATGCTATCAAAAGGAGA 132

Qy 190 aaagaagcttaagaccagcagagaggaagtaacccagcctcaactcagcttgacctaa 249
Dy 133 GGAAGAAGTCCAAAGACAAAGCGCAGCTGAGCCCCAGCCTCGGCTCAGCTTGACCTAA 192

Qy 250 aggcctcagaagattgccaa-ctctatgacgacaatctcggaggctt 298
Dy 193 AGGCCTCAGGAAGTTACCTAAGCTTTATGTGACATTCCTCCCTGAGCTT 242

RESULT 7
AF059030
LOCUS AF059030 5905 bp mRNA ROD 16-JUL-2001
DEFINITION Rattus norvegicus voltage-gated Na channel alpha subunit Nan mRNA, complete cds.
ACCESSION AF059030
VERSION AF059030.2 GI:14719821
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 5905)
AUTHORS Dib-Hajj,J.S.D., Tyrrell,L., Black,J.A. and Waxman,S.G.
TITLE Nan, a novel voltage-gated Na channel, is expressed preferentially in peripheral sensory neurons and down-regulated after axotomy
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (15), 8963-8968 (1998)
MEDLINE 98338024
REFERENCE 2 (bases 1 to 5905)
AUTHORS Dib-Hajj,J.S.D., Tyrrell,L., Black,J.A. and Waxman,S.G.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1998) Neurology, Yale University Medical School, 333 Cedar St., New Haven, CT 06510, USA
COMMENT On Jul 16, 2001 this sequence version replaced gi:3372614.
FEATURES
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location/Qualifiers
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5'UTR
CDS

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1300 a 1338 c 1314 g 1382 t
BASE COUNT
ORIGIN

Query Match 53.5%; Score 160; DB 10; Length 5905;
Best Local Similarity 84.2%; Pred. No. 2.4e-38;
Matches 192; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

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Qy 132 cctctcactccgactctctgctgcaattgagaagcgattgccatccaaaggagaa 191
Dy 103 CCCCTCCTTCCGACTCTCTGCTGCCATAGAGAAGCGGATGCTATCCAAAGGAGAGG 162

Qy 192 aagaagtctaaagaccagacagaggaagtaaccagcagctcaactcagcttgacctaaag 251
Dy 163 AAGAAGTCCAAAGACAAAGCGGCGACGTGAGCCCCAGCCTCGGCTCAGCTTGACCTAAAG 222

Qy 252 gcctccaggaagttgcccac-ctctatggcgacaatcctcggaggctt 298
Dy 223 GCCTCAGGAAGTTACCTAAGCTTTATGCTGACATTCCTCCCTGAGCTT 270

RESULT 8
AF118044
LOCUS AF118044 5858 bp mRNA ROD 07-SEP-1999
DEFINITION Mus musculus voltage-gated sodium channel Nan (Scnlla) mRNA, complete cds.
ACCESSION AF118044
VERSION AF118044.1 GI:5833119
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5858)
AUTHORS Dib-Hajj,J.S.D., Tyrrell,L., Escayg,A., Wood,P.M., Meisler,M.H. and Waxman,S.G.
TITLE Coding sequence, genomic organization, and conserved chromosomal localization of the mouse gene Scnlla encoding the sodium channel Nan
JOURNAL Genomics 59 (3), 309-318 (1999)
MEDLINE 99375324
PUBMED 10444332
REFERENCE 2 (bases 1 to 5858)
```

AUTHORS
TITLE
JOURNAL

Dib-Hajj, S.D., Tyrell, L. and Waxman, S.G.
Direct Submission
Submitted (05-JAN-1999) Neuroscience Research Center, 127A, Yale
University/VAMC, 950 Campbell Ave, West Haven, Ct 06516, USA

FEATURES

source

Location/Qualifiers

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BASE COUNT 1509 a 1436 c 1372 g 1541 t

ORIGIN

Query Match

Best Local Similarity 53.2%; Score 159.2; DB 10; Length 5858;

Matches 193; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

Qy 60 gtctctgtcctgaggggtaagatgagacagatgctaccagatgctaccagatgag 119

Dy 32 GTGCTGAGCAAGGGTGAAGATGAGAGAGGACTATCCAGTGATCTTCCACAGCAG 91

Qy 120 cggatttcgccttcacttcgactctgctgactgcaattgagagcgatgcccac 179

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Qy 180 caaag 239

Dy 152 CAAAAGGAG 211


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ORIGIN
Query Match 50.5%; Score 151; DB 10; Length 5849;
Best Local Similarity 83.6%; Pred. No. 1.4e-35;
Matches 183; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
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Db 1 ATGGAGGAGAGGATCTACCCGGTGATCTCCGGACGAGCGGAATTTCCGCCCTTCACT 60
Qy 141 tccgactctgctgcaattgagaagcgattgccatccaaagagagaaagaaagtct 200
Db 61 TCCGACTCTGCTGCTGATGAGAGCGGATGCTATCCAAAAGGAGAGGAAGATCC 120
Qy 201 aaagaccacagagagagagagagagagagagagagagagagagagagagagagag 260
Db 121 AAAGACAGGCGGAGCTGAGCCCGAGCTCGGCTCGCTGACCTTGACCTAAGAGCCTCCAG 180
Qy 261 aagttgcccac-cctatggcgacacatcctcgaggctt 298
Db 181 AAGTTACCTAAGCTTTATGGTGACATTCCTCCCTGAGCTT 219
RESULT 12
AF117907 5874 bp mRNA PRI 18-MAY-1999
LOCUS Homo sapiens tetrodotoxin-resistant voltage-gated sodium channel
DEFINITION (SCN10A) mRNA, complete cds.
ACCESSION AF117907
VERSION AF117907.1 GI:4838144
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5874)
Rabert,D.K., Koch,B.D., Ilnicka,M., Obernolte,R.A., Naylor,S.L.,
Herman,R.C., Eglen,R.M., Hunter,J.C. and Sangameswaran,L.
A tetrodotoxin-resistant voltage-gated sodium channel from human
dorsal root ganglia, hPN3/SCN10A
Pain 78 (2), 107-114 (1998)
990533555
2 (bases 1 to 5874)
Rabert,D.K., Koch,B.D., Ilnicka,M., Obernolte,R.A., Naylor,S.L.,
Herman,R.C., Eglen,R.M., Hunter,J.C. and Sangameswaran,L.
Direct Submission
Submitted (05-JAN-1999) Target Identification, Roche Bioscience,
3401 Hillview, Palo Alto, CA 94304, USA
FEATURES
Location/Qualifiers
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BASE COUNT 1434 a 1552 c 1428 g 1460 t

ORIGIN

Query Match 15.3%; Score 45.8; DB 9; Length 5874;
Best Local Similarity 60.7%; Pred. No. 0.0031;
Matches 99; Conservative 0; Mismatches 52; Indels 12; Gaps 1;

Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics
 Center project name: H_DA0091H08
) -----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 14 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/OTB/CHRL4>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-6, prepared by Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics, 6:84-9 (1994). The library is from one female donor. For further details, see <http://bacpac.med.buffalo.edu/>. The clone is available from Genome Systems, Inc. (<http://www.genomesystems.com>).

VECTOR:

PPAC4

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP1-261D10; the clone sequenced to the right is RP3-1103L11, 200 bp overlap. Actual start of this clone is at base position 1 of RP6-91H8; actual end is at base position 128202 of RP6-91H8.

FEATURES

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Wed Feb 27 09:58:48 2002

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VERSION	A58859 A58859
KEYWORDS	A58859.1 GI:3714380
SOURCE	.
ORGANISM	unidentified. unidentified unclassified.
REFERENCE	1 (bases 1 to 6527)
AUTHORS	Wood,J.J.N. and Akopian,A.N.
TITLE	ION CHANNEL
JOURNAL	Patent: WO 9701577-A 7 16-JAN-1997; UNIV LONDON (GB)
	PAT
	06-MAR-1998

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BASE COUNT
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	Query Match	12.8%	Score 38.4	DB 6	Length 6527	
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DB	237	AATTTTCAGACGGTTCACTCCAGAGTCACTGGCAGAGATCGAAGACGAGATTGCTGCTCAC	296			
QY	183	aaggagaataaagaagtctaaagaccagacaggagaa	218			
DB	297	CGGGCAGCCCAAGAAGGCCAGAACCAACACACAGGA	332			

Search completed: February 26, 2002, 22:39:29
Job time: 17324 sec

And the first of these is the fact that the world is not a flat plane, but a sphere.

And the second is the fact that the world is not a flat plane, but a sphere.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 22:49:44 ; Search time 478.33 Seconds
(without alignments)
535.907 Million cell updates/sec

Title: US-09-646-224A-3

Perfect score: 299

Sequence: 1 atctaggcaggtgtttt.....cgacaatctcggaggcttt 299

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299	100.0	299	AAZ21481	Human sensory neur
2	204.4	68.4	5860	AAF30101	Human sodium chann
3	167.8	56.1	5908	AAZ60241	CDNA encoding type
4	160.4	53.6	5334	AAZ60244	Stabilised cDNA en
5	160	53.5	5875	AAZ87600	Rat sodium channel
6	160	53.5	5875	AAZ30102	Rat sodium channel
7	158.4	53.0	5897	AAZ21480	Rat sensory neuron
8	157.8	52.8	5822	AAZ87601	Mouse sodium chann
9	157.8	52.8	5822	AAZ30103	Mouse sodium chann
10	45.8	15.3	5874	AAZ57016	Human hPN3 cDNA se
11	44.2	14.8	6606	AAZ60872	NaNG polypeptide e

12	38.4	12.8	6527	18	AAZ77806	CDNA encoding vari
13	38.4	12.8	7052	18	AAZ77805	CDNA encoding vari
14	37.8	12.6	6344	22	AAF57009	Rat PN3 CDNA seque
15	36.8	12.3	6524	18	AAZ77803	CDNA encoding wild
16	34.6	11.6	6729	20	AAZ12974	Enterococcus faeca
17	33	11.0	7608	16	AAZ74118	DNA encoding mouse
18	32.8	11.0	1458	22	AAZ90931	C. elegans UNC-5 c
19	32.8	11.0	1593	22	AAZ90930	C. elegans UNC-5 c
20	32.4	10.8	1932	22	AAZ03528	Human nicotinic ac
21	31.6	10.6	3219	21	AAZ95276	Murine I kappa B k
22	31.6	10.6	8378	22	AAZ55763	Human adult form o
23	31.6	10.6	8378	22	AAZ55764	Human neonatal for
24	31.4	10.5	483	22	AAZ55766	Human SCN1A genom
25	31	10.4	855	19	AAZ52378	Streptococcus pneu
26	31	10.4	13425	19	AAZ52284	Streptococcus pneu
27	30.4	10.2	481	20	AAZ06952	Rice cyclopropane
28	30.4	10.2	1951	22	AAZ92291	Human pollinosis-a
29	30.4	10.2	3442	22	AAZ92313	Human pollinosis-a
30	30.4	10.2	6513	17	AAZ33238	Drosophila para vo
31	30.4	10.2	6513	17	AAZ18986	Drosophila para vo
32	30.4	10.2	6519	20	AAZ82500	Calcium permeable
33	30.2	10.1	1025	22	AAZ55828	Human SCN3A genom
34	30.2	10.1	1066	19	AAZ53410	DNA encoding a bio
35	30.2	10.1	9112	22	AAZ55823	Human adult form o
36	30.2	10.1	9112	22	AAZ55824	Human neonatal for
37	29.8	10.0	558	22	AAZ10196	Human cDNA clone (
38	29.8	10.0	4054	20	AAZ13188	Enterococcus faeca
39	29.6	9.9	531	21	AAZ69707	Human ovarian carc
40	29.6	9.9	2142	22	AAZ15254	Human cDNA sequenc
41	29.6	9.9	2198	22	AAZ14344	Human cDNA sequenc
42	29.6	9.9	2392	20	AAZ61221	Mouse DNA demethyl
43	29.4	9.8	3834	22	AAZ01281	Human alpha nicoti
44	29	9.7	1074	20	AAZ00427	Human secreted pro
45	29	9.7	1297	22	AAZ02555	Human secreted pro

ALIGNMENTS

RESULT 1

1D AAZ21481 standard; cDNA; 299 BP.
AC AAZ21481;
AC AAZ21481;
DT 03-DEC-1999 (first entry)
XX Human sensory neurone specific 2a nucleotide sequence fragment #1.
DE Human sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;
XX Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;
KW voltage gated; hypersensitivity; ss.
XX Homo sapiens.
XX WO9947670-A1.
XX 23-SEP-1999.
XX 18-MAR-1999; 99WO-GB00838.
XX 18-MAR-1998; 98GB-0005793.
XX (GLAX) GLAXO GROUP LTD.
XX Grose DT, Hick CA, Tate SN;
XX WPI; 1999-562112/47.
XX Mammalian sodium channel protein for treating pain and hypersensitivity
XX Claim 6; Page 66; 73pp; English.
XX AAZ21481 to AAZ21495 represent fragments of the human sensory neurone

CC specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel
 CC protein. SNS-2a can be used in a method for the identification of a
 CC modulator of a sodium channel, and for assaying for compounds which
 CC modulate sodium flux. The sodium channel modulators can be used in a
 CC medicament for the treatment of pain or hypersensitivity.

XX
 SQ Sequence 299 BP; 74 A; 81 C; 73 G; 71 T; 0 other;

Query Match 100.0%; Score 299; DB 20; Length 299;
 Best Local Similarity 100.0%; Pred. No. 4.4e-87;
 Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 atcttaggcaggctgtttattcccgctctctgagcgtttcttgagatctgtggcttg 60
 Qy 61 tctctgtctgaggtgagatgatgacagatgctaccagtaattcttccagatgagc 120
 Db 61 tctctgtctgaggtgagatgatgacagatgctaccagtaattcttccagatgagc 120
 Qy 121 ggaatttccgcttccacttccgactctctggtgcaattgagaagcggattgccatcc 180
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RESULT 2

AAF30101
 ID AAF30101 standard; cDNA; 5860 BP.

XX
 AC AAF30101;

XX
 DT 30-APR-2001 (first entry)

XX
 XX Human sodium channel NaN cDNA.

XX
 KW Sodium channel; NaN; human; tetrodotoxin resistant; pain;
 KW paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy;
 KW diagnosis; ss.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT CDS 31..5402
 FT /*tag= a

XX
 PN WO200105831-A1.

XX
 PD 25-JAN-2001.

XX
 PF 14-JUL-2000; 2000WO-US19342.

XX
 PR 16-JUL-1999; 99US-0354147.

XX
 PA (UYIA) UNIV YALE.

XX
 FI Dib-Hejj S, Waxman SG;

XX
 DR WPI; 2001-103147/11.

XX
 DR P-PSDB; AAB20121.

XX
 PT Nucleic acid molecules encoding human tetrodotoxin resistant sodium
 PT channels, useful for preventing, diagnosing and treating pain,
 PT paraesthesia and/or hyperexcitability phenomena -

XX

PS Claim 1; Fig 11A; 162pp; English.

XX The present sequence is that of cDNA encoding a novel human
 CC tetrodotoxin resistant sodium channel, termed NaN (see AAB20121).
 CC The cDNA was isolated from a human dorsal root ganglia tissue cDNA
 CC library by PCR amplification (see also AAF30122-23). NaN belongs
 CC to the a-subunit voltage-gated sodium channel protein family and
 CC produces a TTX-R sodium current. Such channels underlie the
 CC generation and propagation of impulses in excitable cells such as
 CC neurons and muscle fibres. Preferential expression of NaN on
 CC sensory neurons innervating the body (dorsal root ganglia) and the
 CC face (trigeminal ganglia), but not on other neurons, makes it a
 CC very useful target for diagnostic and/or therapeutic uses in
 CC relation to acute and/or chronic pain pathologies. A claimed
 CC method of treating pain, paraesthesia and/or hyperexcitability
 CC phenomena in a human or animal subject involves administering an
 CC agent that alters sodium current flow through NaN channels, or
 CC which modulates transcription or translation of NaN mRNA, in
 CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids
 CC are used in gene therapy to correct disorders associated with
 CC decreased sodium channel expression or (antisense) to down-regulate
 CC NaN expression, in the diagnosis of disease, and in the recombinant
 CC production of NaN polypeptides.

XX Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 other;

Query Match 68.4%; Score 204.4; DB 22; Length 5860;
 Best Local Similarity 96.9%; Pred. No. 6.5e-56;
 Matches 219; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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 Db 73 ggggtgaagatggatgacagatgctaccagtaattcttccagatgagcggaattccgcc 82
 Qy 133 ccttcacttccgactctctgctgcaattgagaagcggatggcattccaaaggagaaaa 192
 Db 133 ccttcacttccgactctctgctgcaattgagaagcggatggcattccaaaggagaaaa 142
 Qy 193 agaagctaaagaccagacagagagaagtacccagcctcaacctcagcttgacctaaagg 252
 Db 143 agaagctaaagaccagacagagagaagtacccagcctcgccctcagcttgacctaaagg 202
 Qy 253 cctcaggaagtgtcccaa-ctctatggcgacaattcttcggaggct 297
 Db 203 cctcaggaagtgtcccaaagctctatggcgacaattcttcggaggct 248

RESULT 3

AAX60241

ID AAX60241 standard; cDNA; 5908 BP.

XX
 AC AAX60241;

XX
 DT 11-AUG-1999 (first entry)

XX
 DE cDNA encoding type 5 sodium channel protein designated PN5.

XX Type 5 sodium channel; PN5; nervous system; plexiform;
 KW dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
 KW diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
 KW neuropathic pain; migraine; headache; ss.

XX
 OS Rattus sp.

XX
 PN FR2771103-A1.

XX
 PD 21-MAY-1999.

XX
 PF 19-NOV-1998; 98FR-0014551.

XX
 PR 20-NOV-1997; 97US-0066225.

XX

CC while not affecting other nerve cells in the brain and spinal cord.
CC The gene encoding Nan has been named Scnlla.
XX
XX
SQ Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 61 other;

Query Match 52.8%; Score 157.8; DB 20; Length 5822;
Best Local Similarity 83.4%; Pred. No. 7.7e-41;
Matches 191; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

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QY	123	aatttcgccccctcaacttccgactctctggctgcgaattgagaagcggattgccatccaa	182
Db	61	aatttcgccccctcaacttccgactcttggctgcgaatgagaagcggatccatccaa	120
QY	183	aaggagaaaaagaagtctaaagaccagacaggaagtagtccccagctcaactcagctt	242
Db	121	aaggagaagaagaatcccaagaagcagcaactgagccccagcctggcctcagctc	180
QY	243	gacctaaaggcctccagggaagtgtgccaa-ctctatggcgacaatctc	290
Db	181	gacctaaaggcctccagggaagttaacctaaagctctatggcagcgttcccc	229

RESULT 9
AAAF30103
ID AAF30103 standard; cDNA; 5822 BP.

AA	
AC	AAF30103;
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Mouse sodium channel NAN cDNA.

Sodium channel; NaN; Scn1a; mouse; tetradotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.

OS	Mus musculus.	Location/Qualifiers
XX	Key	19..5316
FF	CDS	/*tag= a
FT		5789..5794
FT	polyA_signal	/*tag= b
FT		5800..5822
FT	polyA_site	/*tag= c

AA
PN
WO200105831-A1.

25-JAN-2001.

14-JUL-2000: 2000WO-US19342

XX 16-JUL-1999: 99US-0354147.

XX PA (UYYA) UNTV YALF.

XX PI Dib-Hatt S. Waxman SG:

XX
DR WPT: 2001-103147/11

DR
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PT

PS Example 3; Fig 7A; 162pp; English.

CC The present sequence is that of cDNA encoding a novel mouse

tetrodotoxin resistant sodium channel, termed NaN (see AAB20124). The cDNA was isolated from trigeminal ganglia cDNA using primers (see AAT30120-21) based on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN (see AAB20121). The gene encoding NaN, termed Schlla, is located on mouse chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant production of NaN polypeptides.

```

: Query Match          52.8%; Score 157.8; DB 22; Length 5822;
: Best Local Similarity 83.4%; Pred. No. 7.7e-41;
: Matches 191; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

```

Qy 63 tctgtcctgaggggtgaagatggatgacagatgctaccacgtaatctttccaqatgaqcqg 122

Db 1 tctgaaccaagqqtgaagatqgaaggaagqqtactatccagtgatcttccagacgaag 60

QY 123 aatttcqcccccttcacttcqqaactctctqqaacttcaaatcgaagcgaattgccatccaa 182

61 aatttccqcccccttcacttttcqactctttgqctqcaatagagaaagcggatcaccatccaa 120

183 aaaggagaaaaagaaagtctaaagaccagacagagaaagtaccccaacctcaacctcagcctt 242

121 aaggagaaagaaatccaaaagacaaagacagcaactgaaccccaacccagacctcagactc 180

243 gaacctaaaggccctccaggaagtggccaa-ctctatgcccacaaatccctc 380

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RESULT 10

AA57016
ID AAF57016 standard; cDNA; 5874 BP.

AA
AC AAF57016:

14-MAY-2001 (first entry)

Human hPN3 cDNA sequence

XX	Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;
KW	tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PNS; human;
KW	sodium channel protein; peripheral nervous system; allodynia; neuropathy;
KW	hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulneryary;
KW	analgesic; anti-HIV; ss.

XX
CS Homo sapiens.

AA	Key	Location/Qualifiers
PH	CDS	1..5871
FT		/*tag= a
FT		/product= "hpn3"
FT		

PN US6184349-B1.

06-FEB-2001.

2. XX

mutation 1096
 /tag= d
 /label= C>T
 /note= "Causes Ser > Phe substitution"
 mutation 1984
 /tag= e
 /label= G>C
 /note= "Causes His > Asp substitution"
 mutation 1965
 /tag= f
 /label= C>G
 /note= "Causes Thr > Ser substitution"
 mutation 2472
 /tag= g
 /label= A>T
 /note= "Causes Thr > Ser substitution"
 mutation 2986
 /tag= h
 /label= G>T
 /note= "Causes Ser > Ile substitution"
 mutation 3019
 /tag= i
 /label= A>G
 /note= "Causes His > Arg substitution"
 mutation 3158
 /tag= j
 /label= C>T
 /note= "Causes Arg > Thr substitution"
 mutation 3525
 /tag= k
 /label= C>G
 /note= "Causes His > Asp substitution"
 mutation 3556
 /tag= l
 /label= G>C
 /note= "Causes Arg > Thr substitution"
 mutation 5893
 /tag= m
 /label= T>G
 /note= "Causes Ile > Ser substitution"
 mutation 6525.6527
 /tag= n
 /note= "Addition of AAA"

WO9701577-A1.
 16-JAN-1997. 96WO-GB01523.
 25-JUN-1996; 96WO-GB01523.
 28-JUN-1995; 95GB-0013180.
 (UNLO) UNIV COLLEGE LONDON.
 Akopian AN, Wood JN;
 WPI; 1997-100165/09.
 P-PSDB; AAW21740.
 New isolated mammalian sensory neuron sodium channel protein - used to identify modulators of the sodium channel, partic. for the treatment of pain
 Claim 9; Page 85-93; 128pp; English.
 The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This

sequence contains 12 nucleotide differences to the wildtype rat DRG(SNS-B) (see also AAT77803) causing nine amino acid changes.
 Sequence 6527 BP; 1542 A; 1863 C; 1663 G; 1459 T; 0 other;
 Query Match 12.8%; Score 38.4; DB 18; Length 6527;
 Best Local Similarity 62.5%; Pred. No. 0.035;
 Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 123 aatttcgccccttcaattccgactctctgctgcaattgagaagcgattgccaatcaa 182
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |
 237 aatttcagacggttcaactccagatgctcactgagagatcgagaagcagattgctgtcac 296
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |
 183 aaggagaaaaaagagtcttaagaccagacagagagaa 218
 || ||||| | | | || |||||
 297 cgggagcaagaaggccagacccaagcacagagaga 332

RESULT 13

AAT77805

ID AAT77805 standard; cDNA; 7052 BP.

XX AC AAT77805;

XX UT 09-OCT-1997 (first entry)

XX XX cDNA encoding variant rat DRG (SNS-B) #2.

Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin; modulator; impulse; sensory neuron; acute pain; chronic pain; neuropathic pain; glia; muscle; parasympathetic nervous system; enteric nervous system; central nervous system; dorsal root ganglia; ss.
 Rattus rattus.

Key Location/Qualifiers

CDS 204...6602

FT /*tag= a

FT /product= Variant_Rat_DRG(SNS-B)

XX WO9701577-A1.

XX 16-JAN-1997.

XX 25-JUN-1996; 96WO-GB01523.

XX 28-JUN-1995; 95GB-0013180.

XX (UNLO) UNIV COLLEGE LONDON.

XX Akopian AN, Wood JN;

XX WPI; 1997-100165/09.

XX P-PSDB; AAW21739.

XX New isolated mammalian sensory neuron sodium channel protein - used to identify modulators of the sodium channel, partic. for the treatment of pain

XX Claim 9; Page 69-78; 128pp; English.

XX The sequences given in AAT77803-06 encode the wild type and three variant forms of a rat sensory neuron sodium channel protein which is insensitive to tetrodotoxin. The proteins can be used for identifying modulators of the sodium channel. Blockers of the sodium channel will block or prevent the transmission of impulses along sensory neurons and thereby be useful in the treatment of acute, chronic or neuropathic pain. The novel protein is found only in sensory neurons and not in glia, muscle or the neurons of the (para)sympathetic, enteric or central nervous system. The protein is found preferably in the neurons of the dorsal root ganglia or cranial ganglia. This

CC sequence encodes a 2132 amino acid protein that contains a 176 amino
 CC acid repeat inserted after amino acid 585 of wildtype rat DRG(SNS-B)
 CC (see also AAW21737).

SQ Sequence 7052 BP; 1655 A; 2009 C; 1795 G; 1593 T; 0 other;

Query Match 12.8%; Score 38.4; DB 18; Length 7052;
 Best Local Similarity 62.5%; Pred. No. 0.036;
 Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Oy 123 aatttcgcccctcactctcgtcgtcgtcgaattgagaagcgattgccaacaa 182
 ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 237 aatttcagcgttcactccagagtcactggtcagagatcgagaagcagattgctgtcac 296
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Oy 183 aaggagaaaagaagtctaaagaccagacagagagaa 218
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 297 cggcagccaagaaggccagaaccaagcacagagga 332

RESULT 14
 AAF57009 standard; cDNA; 6344 BP.

XX AAF57009;

DT 14-MAY-2001 (first entry)

XX Rat PN3 cDNA sequence.

XX Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit;
 KW tetrodotoxin; TRX; peripheral nerve sodium channel type 3; PN3; rat;
 KW sodium channel protein; peripheral nervous system; allodynia; neuropathy;
 KW hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerary;
 KW analgesic; anti-HIV; ss.

XX Rattus sp.

XX Key Location/Qualifiers
 FH 23..5893
 CDS /*tag= a
 FT /product= "PN3"

XX US6184349-B1.

XX 06-FEB-2001.

XX 15-APR-1997; 97US-0843417.

XX 11-OCT-1995; 95US-0511828.

XX (SYNT) SYNTX USA INC.

PI Herman R, Delgado SG, Fish LM, Sangameswaran L, Rabert DK;

XX WPI; 2001-202004/20.

DR P-PSDB; AAB61995.

PT New rat and human tetrodotoxin-resistant, voltage-gated sodium channel
 PT proteins, present in peripheral nerve tissue, useful as a therapeutic
 PT target for compounds treating peripheral nervous system disorders

PS Example 2; Fig 1A-I; 86pp; English.

XX The invention provides purified and isolated rat and human peripheral
 CC nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins.
 CC The rat peripheral nerve sodium channel type 3 (PN3) protein or its human
 CC homologue are useful for the development of antibodies against PN3 which
 CC are useful in affinity chromatography to purify recombinant sodium
 CC channel proteins or polypeptides, or as a research tool. The PN3 proteins
 CC are useful as therapeutic targets for compounds to treat disorders of the
 CC peripheral nervous system such as allodynia, hyperalgesia, diabetic
 CC neuropathy, traumatic injury and acquired immunodeficiency syndrome

CC (AIDS)-associated neuropathy. The present sequence represents the cDNA
 CC encoding the rat PN3 protein.

SQ Sequence 6344 BP; 1487 A; 1823 C; 1622 G; 1412 T; 0 other;

Query Match 12.6%; Score 37.8; DB 22; Length 6344;
 Best Local Similarity 57.7%; Pred. No. 0.053;
 Matches 94; Conservative 0; Mismatches 57; Indels 12; Gaps 1;

Oy 123 aatttcgcccctcactctcgtcgtcgtcgaattgagaagcgatt----- 173
 ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 56 aatttcagcgttcactccagagtcactggtcagagatcgagaagcagattgctgtcac 115
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Oy 174 ---gcattcccaaaagagaaaagaagtctaaagaccagacagagagaagtaaccagacct 230
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 116 cgcgcagccaagaagccagaaccaagcacagagacagagaggaacaaagggcgagaagccc 175
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||

Oy 231 caactcagcttgacctaaaggctccagggaagtgtgccaact 273
 ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 176 aggcctcagctggacttgaaagcctgtaaccagctgccaagt 218

RESULT 15

AAAT77803

DT AAT77803 standard; cDNA; 6524 BP.

AC AAT77803;

DT 09-OCT-1997 (first entry)

XX cDNA encoding wild type rat DRG (SNS-B).

Rat; sensory neuron sodium channel protein; insensitive; tetrodotoxin;
 modulator; impulse; sensory neuron; acute pain; chronic pain;
 neuropathic pain; glia; muscle; parasympathetic nervous system;
 enteric nervous system; central nervous system; dorsal root ganglia;
 cranial ganglia; ss.

XX Rattus rattus.

XX Key Location/Qualifiers
 FH 204..6077
 CDS /*tag= a
 FT /product= Rat_DRG(SNS-B)

XX WO9701577-A1.

XX 16-JAN-1997.

XX 25-JUN-1996; 96WO-GB01523.

XX 28-JUN-1995; 95GB-0013180.

XX (UNLO) UNIV COLLEGE LONDON.

PI Akopian AN, Wood JN;

XX WPI; 1997-100165/09.

DR P-PSDB; AAW21737.

PT New isolated mammalian sensory neuron sodium channel protein - used
 PT to identify modulators of the sodium channel, partic. for the
 PT treatment of pain

PS Claim 9; Page 50-58; 128pp; English.

XX The sequences given in AAT77803-06 encode the wild type and three
 CC variant forms of a rat sensory neuron sodium channel protein which
 CC is insensitive to tetrodotoxin. The proteins can be used for
 CC identifying modulators of the sodium channel. Blockers of the
 CC sodium channel will block or prevent the transmission of impulses
 CC along sensory neurons and thereby be useful in the treatment of acute,

CC chronic or neuropathic pain. The novel protein is found only in sensory
 CC neurons and not in glia, muscle or the neurons of the (para)sympathetic,
 CC enteric or central nervous system. The protein is found preferably in
 CC the neurons of the dorsal root ganglia or cranial ganglia.

xx
 SQ Sequence 6524 BP; 1540 A; 1866 C; 1662 G; 1456 T; 0 other;

Query Match 12.38; Score 36.8; DB 18; Length 6524;
 Best Local Similarity 61.5%; Pred. No. 0.11;
 Matches 59; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 123 aatttcgccccttcaactccgactctctgctgcaattgagaagcgattgccaacaa 182
 ||||| | ||||| | | ||||| | ||||| ||||| ||||| ||

Db 237 aatttcagacggttcaactccagagtcactgacagagatcgagaagcagattgctgtcac 296
 ||||| | ||||| | | ||||| | ||||| ||||| ||

Qy 183 aaggagaaaaaagtctaaagaccagacagagagaa 218
 | ||||| | | | | | | | | | | | | |

Db 297 cgcgcagccaagaaggccagaaccaagcacagagga 332
 | ||||| | | | | | | | | | | | | |

Search completed: February 26, 2002, 22:49:53
 Job time: 15273 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 22:39:38 ; Search time 177.56 Seconds
(without alignments)
381.375 Million cell updates/sec

Title: US-09-646-224A-3
Perfect score: 299
Sequence: 1 atctaggcaggctgtttt.....cgacaatctcgaggctttt 299

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	45.8	15.3	5874	4	US-08-843-417-9	Sequence 9, Appli
2	37.8	12.6	6344	4	US-08-843-417-1	Sequence 1, Appli
3	30.4	10.2	5461	3	US-07-998-289B-7	Sequence 7, Appli
4	30.4	10.2	6513	1	US-08-338-702-7	Sequence 7, Appli
5	30.4	10.2	6513	1	US-08-337-339-7	Sequence 7, Appli
6	30.4	10.2	6513	1	US-08-724-095-7	Sequence 7, Appli
7	30.4	10.2	6513	5	PCT-US95-14262-7	Sequence 7, Appli
8	30.4	10.2	6513	5	PCT-US95-14378-7	Sequence 7, Appli
9	30.4	10.2	6519	2	US-08-808-793-24	Sequence 24, Appl
10	29	9.7	767	4	US-08-998-416-566	Sequence 24, Appl
11	28.8	9.6	6315	2	US-08-808-793-2	Sequence 2, Appli
12	28.8	9.6	6315	3	US-08-772-512A-2	Sequence 2, Appli
13	28.8	9.6	6318	2	US-08-808-793-1	Sequence 1, Appli
14	28.8	9.6	6318	3	US-08-772-512A-1	Sequence 1, Appli
15	28.6	9.6	2174	2	US-08-665-040-1	Sequence 1, Appli
16	28.4	9.5	6452	3	US-08-836-325-9	Sequence 9, Appli
17	28.2	9.4	9370	1	US-08-320-559-27	Sequence 27, Appl
18	28.2	9.4	9370	3	US-08-545-860D-27	Sequence 27, Appl
19	28.2	9.4	9370	5	PCT-US94-04496-27	Sequence 27, Appl
20	28.2	9.4	9391	1	US-08-320-559-25	Sequence 25, Appl
21	28.2	9.4	9391	3	US-08-545-860D-25	Sequence 25, Appl
22	28.2	9.4	9391	5	PCT-US94-04496-25	Sequence 25, Appl
23	28	9.4	434	3	US-08-581-918A-33	Sequence 33, Appl
24	28	9.4	434	4	US-08-346-147B-33	Sequence 33, Appl
25	28	9.4	823	4	US-08-998-416-505	Sequence 505, App
26	28	9.4	1647	1	US-08-198-446B-9	Sequence 9, Appli
27	28	9.4	1647	2	US-08-870-693-9	Sequence 9, Appli

28	28	9.4	2809	1	US-08-484-105-3	Sequence 3, Appli
29	28	9.4	2809	1	US-08-484-106-3	Sequence 3, Appli
30	28	9.4	4237	1	US-07-844-298B-1	Sequence 1, Appli
31	27.8	9.3	1025	4	US-08-643-212-19	Sequence 19, Appl
32	27.8	9.3	1025	4	US-08-643-212-23	Sequence 23, Appl
33	27.8	9.3	1995	1	US-08-425-069-3	Sequence 3, Appli
34	27.8	9.3	1995	2	US-08-317-844B-3	Sequence 3, Appli
35	27.8	9.3	5977	3	US-09-024-020B-1	Sequence 1, Appli
36	27.8	9.3	6007	3	US-09-024-020B-2	Sequence 2, Appli
37	27.8	9.3	6556	3	US-09-024-020B-7	Sequence 7, Appli
38	27.8	9.3	6586	3	US-09-024-020B-43	Sequence 43, Appl
39	27.8	9.3	6826	3	US-09-024-020B-8	Sequence 8, Appli
40	27.6	9.2	1490	4	US-09-197-679A-2	Sequence 2, Appli
41	27.2	9.1	2369	4	US-08-910-925-2	Sequence 2, Appli
42	27.2	9.1	5707	2	US-08-472-809B-8	Sequence 8, Appli
43	27.2	9.1	6345	2	US-08-472-809B-7	Sequence 7, Appli
44	27.2	9.1	9103	1	US-08-466-033-182	Sequence 182, App
45	27.2	9.1	9103	1	US-08-444-733-182	Sequence 182, App

ALIGNMENTS

RESULT 1
US-08-843-417-9
Sequence 9, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843.417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5874 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-843-417-9

Query Match 15.3%; Score 45.8; DB 4; Length 5874;
Best Local Similarity 60.7%; Pred. No. 4.6e-06;

	Query Match	10.2%	Score 30.4;	DB 5;	Length 6513;
	Best Local Similarity	63.9%;	Pred. No. 1.3;		
	Matches 46;	Conservative	0;	Mismatches 26;	Indels 0;
	Gaps	0;			
QY	126	ttcgcgccccttcaccttcgcgactctctgctgcaattgagaagcgattgcatcccaaaag	185		
Db	69	TTCGTCGCCCTTTACCCGCGAATCATTGTGCGAAATCGAAACACGCATTGGCGCTCAACAT	128		
QY	186	gaqaaaaaagaag	197		

```

RESULT      9
US-08-808-793-24
Sequence 24, Application US/08808793
Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingates, Patricia J.
TITLE OF INVENTION: CALCIUM PERME
TITLE OF INVENTION: AND USE THERE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon, Harrave, De

```

Query Match 9.7%; Score 29; DB 4; Length 767; ...

[illegible]

RESULT 11
US-08-808-793-2
Sequence 2, Application US/08808793
Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Query Match	9.6%	Score 28.8;	DB 3;	Length 6315;
Best Local Similarity	52.5%;	Pred. No. 4.8;		
Matches 63;	Conservative	0;	Mismatches	
			57;	Indels 0;
				Gaps 0;

RESULT 13
US-08-808-793-1
Sequence 1, Application US/08080793
Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32

ADDRESS: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.60/034,361
FILING DATE: 24-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,649
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brame, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600

	Matches	63	Conservative	0	Mismatches	57	Indels	0	Gaps	0
Qy	126	ttccgccccctt	acttcg	actctctg	ctgctg	ctgcaatt	gagaagcg	gattgc	catcca	aaag 185
Fb	46	ttcggctccctt	ccacccg	gaatcatt	cttca	aatcga	caacacg	tatcg	tgaacat	gaa 105
Qy	186	gagaaaaa	gaagtcta	agaacc	agacg	agagaga	agatcccc	cagctc	caactc	agtctgac 245

RESULT 15
US-08-665-040-1
Sequence 1, Application US/08665040
Patent No. 5869318
GENERAL INFORMATION:
APPLICANT: ESTIVILL PALLEJA, XAVIER
APPLICANT: FUENTES, JUAN JOSE
APPLICANT: FRITCHARD, MELANIE
TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE
TITLE OF INVENTION: DOWN SYNDROM CRITICAL REGION OF HUMAN CHROMOSOME 21.

TITLE OF INVENTION: CODING FOR A FOLATE-RICH PROTEIN (DSCN1) HADZEL
 TITLE OF INVENTION: EXPRESSED IN FOETAL BRAIN AND IN HEART AND METHOD
 TITLE OF INVENTION: FOR CHARACTERIZING IT.
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LADAS & PARRY
 STREET: 26 WEST 61ST STREET
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10023
 COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1 FOR DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,040
FILING DATE: JUNE 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ES P9501140
FILING DATE: JUNE 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: JANET I. CORD
REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U010815-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
TELEFAX: (212) 246-8959
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2174 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA for mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: human
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: foetal
TISSUE TYPE: Brain
IMMEDIATE SOURCE: gene library of cDNA
LIBRARY: gene library of cDNA from foetal
CLONE: BC-17.8-1 and BC-17.8-2
POSITION IN GENOME:

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MAP POSITION:  z1q22.1-q22.2
FEATURE:
NAME/KEY:  cdna for mRNA, BC-17.8

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; LOCATION: 1..2174
; FEATURE:
; NAME/KEY: untranslated 5'
; LOCATION: 1..48
; FEATURE:
; NAME/KEY: coding sequence
; LOCATION: 49..560
; OTHER INFORMATION: Down Syndrome critical region 1 (DSCR1)
; FEATURE:
; NAME/KEY: DSCR1
; LOCATION: 1..171 PEPTIDES
; IDENTIFICATION METHOD: translation of the DSCR1 sequence.
; OTHER INFORMATION:
; OTHER INFORMATION: - deduced protein
; OTHER INFORMATION: - proline-rich protein domains
; OTHER INFORMATION: - glutamic acid-rich protein domains
; OTHER INFORMATION: - leucine/phenylalanine-rich protein domains
; FEATURE:
; NAME/KEY: untranslated 3'
; LOCATION: 564..2174
; FEATURE:
; NAME/KEY: 2 poly (A)
; LOCATION: 1541..1546 AND 2132..2137
; US-08-665-040-1
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Query Match          9.6%; Score 28.6; DB 2; Length 2174;
Best Local Similarity 59.0%; Pred. No. 3.1;
Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 192 aagaagtctaaagaccagacagaggaagatccccagcctcaaccttcagcttgacctaaag 251
    || || || || || || || || || || || || || || || || || || || || ||
Db 513 AAAAATTATCCAGACCCAGGAGGCGGAGTACACGCCGATCCACCTCAGCTGAACCTGGCAC 572
    || || || || || || || || || || || || || || || || || || || || ||

Qy 252 gcctccaggaagttgccaaactc 274
    || || || || || || || || || || || || || || || || || || || || ||
Db 573 GCGACGAGGAGCGCATTCCAAATC 595
    || || || || || || || || || || || || || || || || || || || || ||
```

Search completed: February 26, 2002, 22:39:47
Job time: 17247 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 20:07:03 ; Search time 5057.4 Seconds
(without alignments)
635.304 Million cell updates/sec

Title: US-09-646-224A-3
Perfect score: 299
Sequence: 1 atcctaggcaggctgtttt.....cgacaatcctcgaggcttt 299

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estfun:*

2: em_esthum:*

3: em_estin:*

4: em_estom:*

5: em_estpl:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_estl:*

11: gb_est2:*

12: gb_htc:*

13: gb_gss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_inv:*

17: em_gss_pln:*

18: em_gss_pro:*

19: em_gss_rod:*

20: em_gss_vrt:*

21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	13.0	491	11	BF600973
2	39	13.0	493	11	BF706700
3	39	13.0	504	10	BE485569
4	39	13.0	532	10	BE752960
5	39	13.0	533	10	AW654550
6	35.2	11.8	366	10	BE685650
7	35.2	11.8	885	13	AQ739595
8	34.6	11.6	400	11	BE663266
9	34.6	11.6	581	10	BE251756
10	34.2	11.4	515	10	AV668453
11	34	11.4	407	10	AA134408
12	33.8	11.3	504	13	AZ017956

13	33.8	11.3	684	10	AL594553
14	33.6	11.2	386	10	BE632098
15	33.4	11.2	591	13	AQ727308
16	33.2	11.1	289	10	BA451462
17	33.2	11.1	546	10	AA544829
18	33.2	11.1	1101	13	CNS016NJ
19	33	11.0	426	10	AW365859
20	33	11.0	437	10	AW365809
21	33	11.0	462	11	BE816689
22	33	11.0	676	10	AU170796
23	33	11.0	695	10	BE053445
24	33	11.0	830	13	CNS03VOW
25	33	11.0	838	11	BF631471
26	33	11.0	911	11	BG443355
27	33	11.0	912	11	BG445436
28	32.8	11.0	314	10	BE520609
29	32.8	11.0	586	10	AU204804
30	32.6	10.9	260	10	AI527318
31	32.6	10.9	443	10	AW214225
32	32.6	10.9	498	13	AZ288737
33	32.6	10.9	674	13	AQ391592
34	32.6	10.9	910	13	CNS05PAI
35	32.6	10.9	967	11	BF571561
36	32.4	10.8	361	11	BF232577
37	32.4	10.8	392	10	AW804539
38	32.2	10.8	327	13	AZ843152
39	32.2	10.8	367	11	BG408173
40	32.2	10.8	443	10	AA982787
41	32.2	10.8	514	11	BG019419
42	32.2	10.8	522	11	BG486913
43	32.2	10.8	595	11	BG555371
44	32.2	10.8	597	10	AW351192
45	32.2	10.8	618	10	AW460583

ALIGNMENTS

RESULT 1

LOCUS	BF600973	491 bp	mrna	EST	25-APR-2001
DEFINITION	265816 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.				
ACCESSION	BF600973				
VERSION	BF600973.1				
KEYWORDS	EST.				
SOURCE	COW.				
ORGANISM	Bos taurus				
REFERENCE	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.				
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR Primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCCTCAGTCACGAC Plate: 39 row: K column: 13				

Seq primer: ATTTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers
1..491
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
129 a 118 c 125 g 119 t

BASE COUNT

ORIGIN

Query Match 13.0%; Score 39; DB 11; Length 491;
Best Local Similarity 54.5%; Pred. No. 1;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 27 gcctctgagcccttctgagatctgtgcttctctctgagggtaagatgat 86

Db 2 CGGGTTTAAACCCGGCTGATAGTGTGACCTGTGTCTCTCTGGATGAATTCCTGCT 61

Qy 87 gacagatctaccagtaattctccagatgagcggaatttcgcccttcacattccgac 146

Db 62 GGGAGATGGACACAGCAGGTTCTCTTGCCTGATAGTGGCTGCCCTTCTCTCCCAAG 121

Qy 147 tctctggctgcaattgagaagcg 169

Db 122 TGAATCCCGCATCTTAAAGTG 144

RESULT 2

BF706700

LOCUS

BF706700 493 bp mRNA EST 25-APR-2001
DEFINITION 281320 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION

BF706700

VERSION

BF706700.1

KEYWORDS

EST.

SOURCE

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 493)

Smith,I.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,

Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett

,G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C.G.,

Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and

Keele,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 78 row: N column: 15

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..493

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

129 a 118 c 126 g 120 t

BASE COUNT

ORIGIN

Query Match 13.0%; Score 39; DB 11; Length 493;

Best Local Similarity 54.5%; Pred. No. 1;

Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 27 gcctctgagcccttctgagatctgtgcttctctctgagggtaagatgat 86

Db 1 CGGGCTTTAAACCCGGCTGATAGTGTGACCTGTGTCTCTCTGGATGAATTCCTGCT 60

Qy 87 gacagatctaccagtaattctccagatgagcggaatttcgcccttcacattccgac 146

Db 61 GGGAGATGGACACAGCAGGTTCTCTTGCCTGATAGTGGCTGCCCTTCTCTCCCAAG 120

Qy 147 tctctggctgcaattgagaagcg 169

Db 121 TGAATCCCGCATCTTAAAGTG 143

RESULT 3

BE485569

LOCUS

DEFINITION

172639 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION

BE485569

VERSION

BE485569.1

KEYWORDS

EST.

SOURCE

cow.

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

Bovidae; Bovinae; Bos.

1 (bases 1 to 504)

Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

Wells,K.D.

Mapping of Expressed Sequence Tags from a normalized bovine mammary

gland cDNA library

Unpublished (2000)

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 133 row: O column: 22

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..504

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="BARC 5BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

BASE COUNT

ORIGIN

133 a 123 c 125 g 123 t

RESULT	7
AQ739595/c	
LOCUS	
DEFINITION	

VERSION
KEYWORDS
SOURCE

REFERENCE AND AUTHORS

ORIGIN

Db 638

Db 518

RESULT 8
HG663266

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